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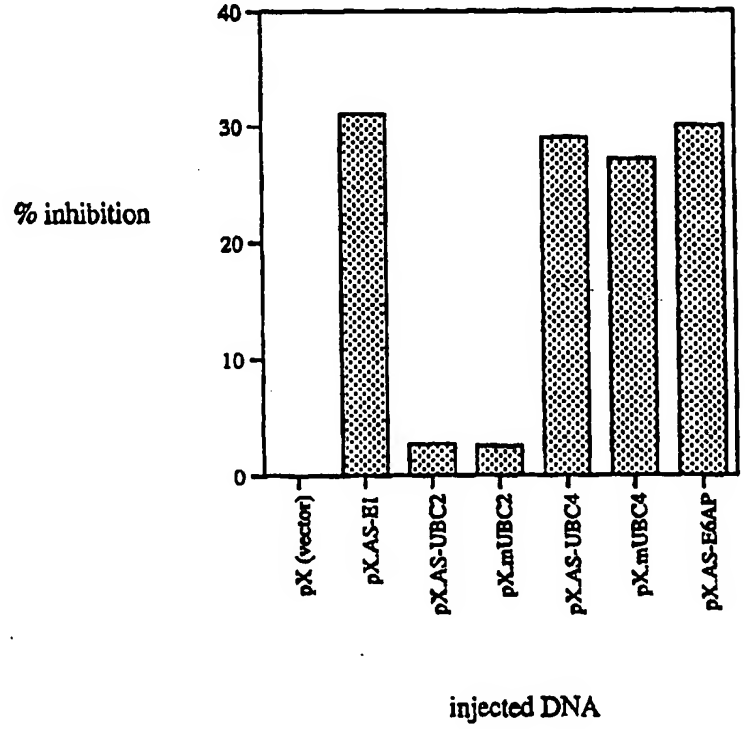
(54) Title: UBIQUITIN CONJUGATING ENZYMES

(57) Abstract

The present invention relates to drug screening assays which provide a systematic and practical approach for the identification of candidate agents able to inhibit ubiquitin-mediated degradation of a cell-cycle regulatory protein, such as p53, p27, myc, fos, MATα2, or cyclins. The invention further relates to novel ubiquitin-conjugating enzymes, and further uses related thereto.



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Ubiquitin Conjugating Enzymes

Background of the Invention

The ubiquitin-mediated proteolysis system is the major pathway for the selective, controlled degradation of intracellular proteins in eukaryotic cells. Ubiquitin modification of a variety of protein targets within the cell appears to be important in a number of basic cellular functions such as regulation of gene expression, regulation of the cell-cycle, modification of cell surface receptors, biogenesis of ribosomes, and DNA repair. One major function of the ubiquitin-mediated system is to control the half-lives of cellular proteins. The half-life of different proteins can range from a few minutes to several days, and can vary considerably depending on the cell-type, nutritional and environmental conditions, as well as the stage of the cell-cycle.

Targeted proteins undergoing selective degradation, presumably through the actions of a ubiquitin-dependent proteosome, are covalently tagged with ubiquitin through the formation of an isopeptide bond between the C-terminal glycyl residue of ubiquitin and a specific lysyl residue in the substrate protein. This process is catalyzed by a ubiquitin-activating enzyme (E1) and a ubiquitin-conjugating enzyme (E2), and in some instances may also require auxiliary substrate recognition proteins (E3s). Following the linkage of the first ubiquitin chain, additional molecules of ubiquitin may be attached to lysine side chains of the previously conjugated moiety to form branched multi-ubiquitin chains.

The conjugation of ubiquitin to protein substrates is a multi-step process. In an initial ATP requiring step, a thioester is formed between the C-terminus of ubiquitin and an internal cysteine residue of an E1 enzyme. Activated ubiquitin is then transferred to a specific cysteine on one of several E2 enzymes. Finally, these E2 enzymes donate ubiquitin to protein substrates. Substrates are recognized either directly by ubiquitin-conjugated enzymes or by associated substrate recognition proteins, the E3 proteins, also known as ubiquitin ligases.

Ubiquitin is itself a substrate for ubiquitination. Depending on the ubiquitin-conjugating enzyme and the nature of the substrate, specific lysine residues of ubiquitin are used as acceptor sites for further ubiquitinations. This can lead to either a linear multi-ubiquitin chain (when a single lysine residue of ubiquitin is used) or multi-ubiquitin "trees" (when more than one lysine reside of ubiquitin is used). Although the attachment of a single ubiquitin moiety to a substrate can be sufficient for degradation, multi-ubiquitination appears to be required in most cases.

Many proteins that control cell-cycle progression are short-lived. For example, regulation of oncoproteins and anti-oncoproteins clearly plays an important role in determining steady-state levels of protein expression, and alterations in protein degradation

are as likely as changes in transcription and/or translation to cause either the proliferative arrest of cells, or alternatively, the transformation of cells.

For instance, the p53 protein is a key regulator of mammalian cell growth and its gene is frequently mutated in a wide range of human tumors (Hollstein et al. (1991) *Science* 253:49-53). Furthermore, many DNA tumor viruses encode viral antigens that inactivate p53 (e.g., see Vogelstein et al. (1992) *Cell* 70:523-526). The high risk human papillomaviruses, such as HPV-16 and -18, are strongly implicated in the pathogenesis of cervical carcinoma (zur Hansen et al. (1991) *Science* 254:1167-1173). These viruses encode two transforming proteins, E6 and E7, that target the cellular growth regulators p53 and pRb respectively. The mode of inactivation of p53 by E6 is apparently mediated by a ubiquitin-dependent pathway. Viral E6 and a cellular E6-associated protein (E6AP) combine to stimulate the ubiquitination of p53, thus targeting p53 for degradation (Scheffner et al. (1990) *Cell* 63:1129-1136. In this reaction, E6 and E6AP are thought to be providing a ubiquitin ligase, or E3-like activity (Scheffner et al. (1993) *Cell* 75:495-505). However, the ubiquitin-conjugating enzyme (E2) involved in p53 ubiquitination has not previously been characterized.

Summary of the Invention

The present invention relates to the discovery of novel ubiquitin conjugating enzymes (hereinafter UBC's, e.g., UbCE's or rapUBC).

One aspect of the present invention relates to the discovery in eukaryotic cells, particularly human cells and certain yeast cells, of a novel ubiquitin conjugating enzyme (hereinafter "UbCE"). In human cells, the enzyme can function to mediate ubiquitination of cell check regulatory proteins, e.g. p53, and is therefore involved in regulating cell cycle progression, e.g. cell growth.

Another aspect of the present invention relates to the discovery in human cells of novel ubiquitin conjugating enzyme (rapUBC), which was discovered based on its ability to bind FKBP/rapamycin complexes. This enzyme can function to mediate ubiquitination of cell check regulatory proteins, e.g. p53, and is therefore involved in regulating eucaryotic cell cycle progression, e.g. cell growth.

Another aspect of the invention features a substantially pure preparation of a human UbCE polypeptide ("hUbCE"), or a fragment thereof, which can function as a ubiquitin conjugating enzyme. In a preferred embodiment: the polypeptide has an amino acid sequence at least 90% homologous to the amino acid sequence of SEQ ID No. 2; the polypeptide has an amino acid sequence at least 95% homologous to the amino acid sequence of SEQ ID No. 2; the polypeptide has an amino acid sequence at least 97% homologous to the amino acid sequence of SEQ ID No. 2; the polypeptide has an amino acid sequence identical to the amino acid sequence of SEQ ID No. 2. In a preferred embodiment: the fragment comprises at least 5 contiguous amino acid residues of SEQ ID No. 2; the fragment

comprises at least 20 contiguous amino acid residues of SEQ ID No. 2; the fragment comprises at least 50 contiguous amino acid residues of SEQ ID No. 2. In a preferred embodiment, the fragment comprises at least a portion of amino acid residues Cys-107 through Met-147, e.g. 5 amino acid residues, e.g. 15 amino acid residues, e.g. 25 amino acid residues.

Another aspect of the invention features a substantially pure preparation of a *Candida* UbCE polypeptide ("caUbCE"), or a fragment thereof, which can function as a ubiquitin conjugating enzyme. In a preferred embodiment: the polypeptide has an amino acid sequence at least 90% homologous to the amino acid sequence of SEQ ID No. 4; the polypeptide has an amino acid sequence at least 95% homologous to the amino acid sequence of SEQ ID No. 4; the polypeptide has an amino acid sequence at least 97% homologous to the amino acid sequence of SEQ ID No. 4; the polypeptide has an amino acid sequence identical to the amino acid sequence of SEQ ID No. 4. In a preferred embodiment: the fragment comprises at least 5 contiguous amino acid residues of SEQ ID No. 4; the fragment comprises at least 20 contiguous amino acid residues of SEQ ID No. 4; the fragment comprises at least 50 contiguous amino acid residues of SEQ ID No. 4. In a preferred embodiment, the fragment comprises at least a portion of amino acid residues Cys-107 through Val-147, e.g. 5 amino acid residues, e.g. 15 amino acid residues, e.g. 25 amino acid residues.

Another aspect of the invention features a substantially pure preparation of a *Schizosaccharomyces* UbCE polypeptide ("spUbCE"), or a fragment thereof, which can function as a ubiquitin conjugating enzyme. In a preferred embodiment: the polypeptide has an amino acid sequence at least 90% homologous to the amino acid sequence of SEQ ID No. 6; the polypeptide has an amino acid sequence at least 95% homologous to the amino acid sequence of SEQ ID No. 6; the polypeptide has an amino acid sequence at least 97% homologous to the amino acid sequence of SEQ ID No. 6; the polypeptide has an amino acid sequence identical to the amino acid sequence of SEQ ID No. 6. In a preferred embodiment: the fragment comprises at least 5 contiguous amino acid residues of SEQ ID No. 6; the fragment comprises at least 20 contiguous amino acid residues of SEQ ID No. 6; the fragment comprises at least 50 contiguous amino acid residues of SEQ ID No. 6. In a preferred embodiment, the fragment comprises at least a portion of amino acid residues Cys-107 through Ile-147, e.g. 5 amino acid residues, e.g. 15 amino acid residues, e.g. 25 amino acid residues.

Another aspect of the invention features a substantially pure preparation of a human UBC polypeptide ("rapUBC"), or a fragment thereof, which can function as a ubiquitin conjugating enzyme. In a preferred embodiment: the polypeptide has an amino acid sequence at least 90% homologous to the amino acid sequence of SEQ ID No. 13; the polypeptide has an amino acid sequence at least 95% homologous to the amino acid sequence

of SEQ ID No. 13; the polypeptide has an amino acid sequence at least 97% homologous to the amino acid sequence of SEQ ID No. 13; the polypeptide has an amino acid sequence identical to the amino acid sequence of SEQ ID No. 13. In a preferred embodiment: the fragment comprises at least 5 contiguous amino acid residues of SEQ ID No. 13; the fragment comprises at least 20 contiguous amino acid residues of SEQ ID No. 13; the fragment comprises at least 50 contiguous amino acid residues of SEQ ID No. 13.

Another aspect of the present invention features an hUbCE polypeptide which functions in one of either role of an agonist of cell-cycle regulation or an antagonist of cell-cycle regulation. In a preferred embodiment the hUbCE polypeptide has: an ability to mediate ubiquitination of cellular proteins, e.g. cell-cycle regulatory proteins, e.g. p53; an ability to mediate ubiquitin-dependent degradation of cellular proteins, e.g. cell-cycle regulatory proteins, e.g. p53; an ability to affect the cellular half-life of a cell-cycle regulatory protein, e.g. a cell-cycle checkpoint protein, e.g. p53, e.g. in normal cells, e.g. in normal proliferating cells, e.g. in virally-infected cells, e.g. in papillomavirus infected cells, e.g. in HPV-infected cells, e.g. in HPV-16, HPV-18, HPV-31, or HPV-33 infected cells, e.g. in cells expressing a papillomavirus E6 protein, e.g. in transformed cells, e.g. in cancerous cells. The biological activity can further include the ability to bind and conjugate ubiquitin, as well as bind and transfer ubiquitin to E6AP.

Another aspect of the present invention features a rapUBC polypeptide which functions in one of either role of an agonist of cell-cycle regulation or an antagonist of cell-cycle regulation. In a preferred embodiment the rapUBC polypeptide has: an ability to bind a FKBP/rapamycin complex, an ability to mediate ubiquitination of cellular proteins, e.g. cell-cycle regulatory proteins, e.g. p53 or p27; an ability to mediate ubiquitin-dependent degradation of cellular proteins, e.g. cell-cycle regulatory proteins, e.g. p53; an ability to affect the cellular half-life of a cell-cycle regulatory protein, e.g. a cell-cycle checkpoint protein, e.g. p53, e.g. in normal cells, e.g. in cancerous cells. Given that rapamycin causes a block in the cell-cycle during G1 phase, it is probable that the spectrum of biological activity of the subject rapUBC enzyme includes control of half-lives of certain cell cycle regulatory proteins, particularly relatively short lived proteins (e.g. proteins which have half-lives on the order of 30 minutes to 2 hours). For example, the subject rapUBC may have the ability to mediate ubiquitination of, for example, p53, p27, myc and/or cyclins, and therefore affects the cellular half-life of a cell-cycle regulatory protein in proliferating cells. The binding of the rapUBC to the FKBP/rapamycin complex may result in sequestering of the enzyme away from its substrate proteins. Thus, rapamycin may intefere with the ubiquitin-mediated degradation of p53 in a manner which causes cellular p53 levels to rise which in turn inhibits progression of the G1 phase.

Yet another aspect of the present invention concerns an immunogen comprising an UBC polypeptide, or a fragment thereof, in an immunogenic preparation, the immunogen

being capable of eliciting an immune response specific for the UBC polypeptide; e.g. a humoral response, eg. an antibody response; e.g. a cellular response.

A still further aspect of the present invention features an antibody preparation specifically reactive with an epitope of the UBC immunogen, e.g., reactive with rapUBC, e.g. reactive with hUbCE, e.g. reactive with caUbC, e.g. reactive with spUbCE.

Another aspect of the present invention features recombinant hUbCE polypeptide, or a fragment thereof, having an amino acid sequence preferably: at least 90% homologous to SEQ ID No. 2; at least 95% homologous to SEQ ID No: 2; at least 97% homologous to SEQ ID No. 2. In a preferred embodiment, the recombinant hUbCE protein functions in one of either role of an agonist of cell cycle regulation or an antagonist of cell cycle regulation. In a more preferred embodiment: the hUbCE polypeptide mediates ubiquitination of cellular proteins, e.g. cell-cycle regulatory proteins, e.g. p53; the hUbCE polypeptide mediates ubiquitin-dependent degradation of cellular proteins, e.g. cell-cycle regulatory proteins, e.g. p53; the hUbCE polypeptide affects the cellular half-life of a cell-cycle regulatory protein, e.g. a cell-cycle checkpoint protein, e.g. p53, e.g. in normal cells, e.g. in normal proliferating cells, e.g. in virally-infected cells, e.g. in papillomavirus infected cells, e.g. in HPV-infected cells, e.g. in HPV-16, HPV-18, HPV-31, or HPV-33 infected cells, e.g. in cells expressing a papillomavirus E6 protein, e.g. in transformed cells, e.g. in cancerous cells.

Another aspect of the present invention features recombinant caUbCE polypeptide, or a fragment thereof, having an amino acid sequence preferably: at least 90% homologous to SEQ ID No. 4; at least 95% homologous to SEQ ID No. 4; at least 97% homologous to SEQ ID No. 4. In a preferred embodiment, the recombinant caUbCE protein functions in one of either role of an agonist of cell cycle regulation or an antagonist of cell cycle regulation. In a more preferred embodiment the caUbCE polypeptide mediates ubiquitination of cellular proteins of *candida* cells.

Another aspect of the present invention features recombinant spUbCE polypeptide, or a fragment thereof, having an amino acid sequence preferably: at least 90% homologous to SEQ ID No. 6; at least 95% homologous to SEQ ID No. 6; at least 97% homologous to SEQ ID No. 6. In a preferred embodiment, the recombinant spUbCE protein functions in one of either role of an agonist of cell cycle regulation or an antagonist of cell cycle regulation. In a more preferred embodiment the spUbCE polypeptide mediates ubiquitination of cellular proteins of *Schizosaccharomyces* cells.

Another aspect of the present invention features recombinant rapUBC polypeptide, or a fragment thereof, having an amino acid sequence preferably: at least 90% homologous to SEQ ID No. 13; at least 95% homologous to SEQ ID No: 13; at least 97% homologous to SEQ ID No. 13. In a preferred embodiment, the recombinant rapUBC protein functions in one of either role of an agonist of cell cycle regulation or an antagonist of cell cycle regulation. In a more preferred embodiment: the rapUBC polypeptide mediates ubiquitination

of cellular proteins, e.g. cell-cycle regulatory proteins, e.g. p53; the rapUBC polypeptide mediates ubiquitin-dependent degradation of cellular proteins, e.g. cell-cycle regulatory proteins, e.g. p53; the rapUBC polypeptide affects the cellular half-life of a cell-cycle regulatory protein, e.g. a cell-cycle checkpoint protein, e.g. p53, e.g. in normal cells, e.g. in cancerous cells.

In yet other preferred embodiments, the recombinant UBC protein is a fusion protein further comprising a second polypeptide portion having an amino acid sequence from a protein unrelated the protein of SEQ ID No. 2, 4, 6 or 13. Such fusion proteins can be functional in a two-hybrid assay.

Another aspect of the present invention provides a substantially pure nucleic acid having a nucleotide sequence which encodes an hUbCE polypeptide, or a fragment thereof, having an amino acid sequence at least 90% homologous to SEQ ID NO. 2. In a more preferred embodiment, the nucleic acid encodes a protein having an amino acid sequence at least 95% homologous to SEQ ID No. 2; and more preferably at least 97% homologous to SEQ ID No. 2. The nucleic preferably encodes: a hUbCE polypeptide which mediates ubiquitination of cellular proteins, e.g. cell-cycle regulatory proteins, e.g. p53; a hUbCE polypeptide which mediates ubiquitin-dependent degradation of cellular proteins, e.g. cell-cycle regulatory proteins, e.g. p53; a hUbCE polypeptide which affects the cellular half-life of a cell-cycle regulatory protein, e.g. a cell-cycle checkpoint protein, e.g. p53, e.g. in normal cells, e.g. in normal proliferating cells, e.g. in virally-infected cells, e.g. in papillomavirus infected cells, e.g. in HPV-infected cells, e.g. in HPV-16, HPV-18, HPV-31, or HPV-33 infected cells, e.g. in cells expressing a papillomavirus E6 protein, e.g. in transformed cells, e.g. in cancerous cells.

Another aspect of the present invention provides a substantially pure nucleic acid having a nucleotide sequence which encodes a caUbCE polypeptide, or a fragment thereof, having an amino acid sequence at least 90% homologous to SEQ ID NO. 4. In a more preferred embodiment, the nucleic acid encodes a protein having an amino acid sequence at least 95% homologous to SEQ ID No. 4; and more preferably at least 97% homologous to SEQ ID No. 4.

Another aspect of the present invention provides a substantially pure nucleic acid having a nucleotide sequence which encodes an spUbCE polypeptide, or a fragment thereof, having an amino acid sequence at least 90% homologous to SEQ ID NO. 4. In a more preferred embodiment, the nucleic acid encodes a protein having an amino acid sequence at least 95% homologous to SEQ ID No. 4; and more preferably at least 97% homologous to SEQ ID No. 4.

Another aspect of the present invention provides a substantially pure nucleic acid having a nucleotide sequence which encodes a rapUBC polypeptide, or a fragment thereof, having an amino acid sequence at least 90% homologous to SEQ ID NO. 13. In a more

preferred embodiment, the nucleic acid encodes a protein having an amino acid sequence at least 95% homologous to SEQ ID No. 13; and more preferably at least 97% homologous to SEQ ID No. 13. The nucleic acid preferably encodes: a rapUBC polypeptide which mediates ubiquitination of cellular proteins, e.g. cell-cycle regulatory proteins, e.g. p53; a rapUBC polypeptide which mediates ubiquitin-dependent degradation of cellular proteins, e.g. cell-cycle regulatory proteins, e.g. p53; a rapUBC polypeptide which affects the cellular half-life of a cell-cycle regulatory protein, e.g. a cell-cycle checkpoint protein, e.g. p53, e.g. in normal cells, e.g. in cancerous cells.

In yet a further preferred embodiment, the nucleic acid which encodes a UBC polypeptide of the present invention, or a fragment thereof, hybridizes under stringent conditions to a nucleic acid probe corresponding to at least 12 consecutive nucleotides of one of SEQ ID Nos. 1, 3, 5 or 12; more preferably to at least 20 consecutive nucleotides of said sequences; more preferably to at least 40 consecutive nucleotides. In yet a further preferred embodiment, the UbCE encoding nucleic acid hybridizes to a nucleic acid probe corresponding to a subsequence encoding at least 4 consecutive amino acids between residues 107 and 147 of SEQ ID No. 2, 4 or 6, more preferably at least 10 consecutive amino acid residues, and even more preferably at least 20 amino acid residues. In yet a preferred embodiment the nucleic acid encodes an hUbCE polypeptide which includes Cys-107 through Cys-111.

Furthermore, in certain preferred embodiments, UBC encoding nucleic acid will comprise a transcriptional regulatory sequence, e.g. at least one of a transcriptional promoter or transcriptional enhancer sequence, operably linked to the UBC gene sequence so as to render the UBC gene sequence suitable for use as an expression vector. In one embodiment, the UBC gene is provided as a sense construct. In another embodiment, the UBC gene is provided as an anti-sense construct.

The present invention also features transgenic non-human animals, e.g. mice, which either express a heterologous hUbCE or rapUBC gene, e.g. derived from humans, or which mis-express their own homolog of the subject human gene, e.g. expression of the mouse hUbCE or rapUBC homolog is disrupted. Such a transgenic animal can serve as an animal model for studying cellular disorders comprising mutated or mis-expressed hUbCE opr rapUBC alleles.

The present invention also provides a probe/primer comprising a substantially purified oligonucleotide, wherein the oligonucleotide comprises a region of nucleotide sequence which hybridizes under stringent conditions to at least 10 consecutive nucleotides of sense or antisense sequence of SEQ ID No. 1 or SEQ ID No:12, or naturally occurring mutants thereof. In preferred embodiments, the probe/primer further comprises a label group attached thereto and able to be detected, e.g. the label group is selected from a group consisting of radioisotopes, fluorescent compounds, enzymes, and enzyme co-factors. Such

probes can be used as a part of a diagnostic test kit for identifying transformed cells, such as for measuring a level of a hUbCE or a rapUBC nucleic acid in a sample of cells isolated from a patient; e.g. measuring the hUbCE or rapUBC mRNA level in a cell; e.g. determining whether the genomic hUbCE or rapUBC gene has been mutated or deleted.

The present invention also provides a method for treating an animal having unwanted cell growth characterized by a loss of wild-type p53 function, comprising administering a therapeutically effective amount of an agent able to inhibit a ubiquitin conjugating activity of the subject hUbCE or rapUBC protein.

The present invention also provides a method for treating an animal having an unwanted mycotic infection, comprising administering a therapeutically effective amount of an agent able to inhibit a ubiquitin conjugating activity of a fungal ubiquitin-conjugating enzyme, such as the subject caUbCE protein or spUBC protein, without substantially inhibiting the hUbCE protein.

Another aspect of the present invention provides a method of determining if a subject, e.g. a human patient, is at risk for a disorder characterized by unwanted cell proliferation, comprising detecting, in a tissue of the subject, the presence or absence of a genetic lesion characterized by at least one of (i) a mutation of a gene encoding a protein represented by SEQ ID No. 2 or SEQ ID No:13, or a homolog thereof; or (ii) the mis-expression of the hUbCE or rapUBC gene. In preferred embodiments: detecting the genetic lesion comprises ascertaining the existence of at least one of a deletion of one or more nucleotides from the gene, an addition of one or more nucleotides to the gene, an substitution of one or more nucleotides of the gene, a gross chromosomal rearrangement of the gene, a gross alteration in the level of a messenger RNA transcript of the gene, the presence of a non-wild type splicing pattern of a messenger RNA transcript of the gene, or a non-wild type level of the protein. For example, detecting the genetic lesion can comprise (i) providing a probe/primer comprising an oligonucleotide containing a region of nucleotide sequence which hybridizes to a sense or antisense sequence of SEQ ID No. 1 or SEQ ID No:12, or naturally occurring mutants thereof or 5' or 3' flanking sequences naturally associated with the gene; (ii) exposing the probe/primer to nucleic acid of the tissue; and (iii) detecting, by hybridization of the probe/primer to the nucleic acid, the presence or absence of the genetic lesion; e.g. wherein detecting the lesion comprises utilizing the probe/primer to determine the nucleotide sequence of the hUbCE or rapUBC gene and, optionally, of the flanking nucleic acid sequences; e.g. wherein detecting the lesion comprises utilizing the probe/primer in a polymerase chain reaction (PCR); e.g. wherein detecting the lesion comprises utilizing the probe/primer in a ligation chain reaction (LCR). In alternate embodiments, the level of the protein is detected in an immunoassay.

The present invention also provides a systematic and practical approach for the identification of candidate agents able to inhibit ubiquitin-mediated degradation of a cell-

cycle regulatory protein, such as p53, p27, myc, fos, MATα2, or cyclins. One aspect of the present invention relates to a method for identifying an inhibitor of ubiquitin-mediated proteolysis of a cell-cycle regulatory protein by (i) providing a ubiquitin-conjugating system that includes the regulatory protein and ubiquitin under conditions which promote the ubiquitination of the target protein, and (ii) measuring the level of ubiquitination of the subject protein brought about by the system in the presence and absence of a candidate agent. A decrease in the level of ubiquitin conjugation is indicative of an inhibitory activity for the candidate agent. The level of ubiquitination of the regulatory protein can be measured by determining the actual concentration of protein:ubiquitin conjugates formed; or inferred by detecting some other quality of the subject protein affected by ubiquitination, including the proteolytic degradation of the protein. In certain embodiments, the present assay comprises an *in vivo* ubiquitin-conjugating system, such as a cell able to conduct the regulatory protein through at least a portion of a ubiquitin-mediated proteolytic pathway. In other embodiments, the present assay comprises an *in vitro* ubiquitin-conjugating system comprising a reconstituted protein mixture in which at least the ability to transfer ubiquitin to the regulatory protein is constituted. Moreover, the present assay may further comprise auxiliary proteins which influence the level of ubiquitin-mediated degradation, including viral oncogenic proteins, such as the E6 protein of high-risk HPVs, which influence the level of the regulatory protein in an infected cell by enhancing or otherwise altering the proteolysis of the protein.

Yet a further aspect of the present invention concerns three-dimensional molecular models of the subject UBC proteins, and their use as templates for the design of agents able to inhibit at least one biological activity of the ubiquitin conjugating enzyme. In preferred embodiments, the molecular models can be used to design pharmacophores by rational drug design; e.g. agents which can inhibit binding of the subject hUbCE or rapUBC protein with any one of ubiquitin, an E1 enzyme, an E3 protein(s) such as E6 or E6AP, or the downstream target of the enzyme, such as p53.

For instance, one aspect of the present invention concerns a method for identifying inhibitors of the subject ubiquitin-conjugating enzyme by molecular modeling. In general, the method comprise providing a molecular model of the enzyme, such as the active site, as well as a molecular model of a candidate drug. The drug model is docked with the UBC model and binding criteria, e.g. electrostatic interactions, hydrogen bonding, hydrophobic interactions, desolvation effects, cooperative motions of ligand and enzyme, of the docked models is determined. Based on the binding criteria of a particular candidate drug, the likelihood of the candidate drug being an inhibitor of said UBC can be determined. Thus, the subject method can be used to design candidate agents, which when obtained, e.g. by chemical synthesis or from commercial sources, can be provided in an assay with the human ubiquitin-conjugating enzyme of the present invention in order to determine the actual

inhibitory activity of the candidate drug. In preferred embodiments, the hUbCE model includes the amino acid residues Cys-85, Leu-86, Asp-87, Ile-88, Arg-90, Ser-91, Leu-109, Asn-114, Asp-116, and Asp-117, the atomic coordinates of these residues, at 300°K, having an overall RMS within 2Å of the atomic coordinates shown in Figure 2, more preferably an overall RMS within 1Å, and most preferably an overall RMS within 0.5Å. Moreover, the hUbCE model can include amino acid residues Arg-5 through Met-147 of SEQ ID No. 2. In preferred embodiments, the atomic coordinates for the C-α carbon for each of these residues, at 300°K, have an overall RMS within 2Å of the C-α atomic coordinates shown in Figure 1, more preferably an overall RMS within 1Å, and most preferably an overall RMS within 0.5Å. Moreover, the hUbCE model can include the atomic coordinates for each atom of the amino acid residues Arg-5 through Met-147 of SEQ ID No. 2. In preferred embodiments, the atomic coordinates for each of these residues, at 300°K, have an overall RMS within 2Å of the C-α atomic coordinates shown in Figure 1, more preferably an overall RMS within 1Å, and most preferably an overall RMS within 0.5Å.

Yet a further aspect of this invention concerns addressable electronic memory means, e.g. RAM or ROM memory, magnetic disk devices, optical storage devices, having stored therein an addressable electronic representation of atomic coordinates of a molecular model of a UBC enzyme. In preferred embodiments, the hUbCE model comprises the amino acid residues Cys-85, Leu-86, Asp-87, Ile-88, Arg-90, Ser-91, Leu-109, Asn-114, Asp-116, and Asp-117, the atomic coordinates of these residues, at 300°K, having an overall RMS within 2Å of the atomic coordinates shown in Figure 2. In another embodiments, the human ubiquitin-conjugating enzyme model comprises amino acid residues Arg-5 through Met-147 of SEQ ID No. 2, the atomic coordinates of the residues, at 300°K, having an overall RMS within 2Å of the atomic coordinates shown in Figure 1.

Other features and advantages of the invention will be apparent from the following detailed description, and from the claims.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of cell biology, cell culture, molecular biology, transgenic biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See, for example, *Molecular Cloning A Laboratory Manual*, 2nd Ed., ed. by Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory Press:1989); *DNA Cloning*, Volumes I and II (D. N. Glover ed., 1985); *Oligonucleotide Synthesis* (M. J. Gait ed., 1984); Mullis et al. U.S. Patent No. 4,683,195; *Nucleic Acid Hybridization* (B. D. Hames & S. J. Higgins eds. 1984); *Transcription And Translation* (B. D. Hames & S. J. Higgins eds. 1984); *Culture Of Animal Cells* (R. I. Freshney, Alan R. Liss, Inc., 1987); *Immobilized Cells And Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide To Molecular Cloning* (1984); the treatise, *Methods In Enzymology* (Academic Press, Inc., N.Y.); *Gene Transfer Vectors For Mammalian Cells* (J. H. Miller and

M. P. Calos eds., 1987, Cold Spring Harbor Laboratory); *Methods In Enzymology*, Vols. 154 and 155 (Wu et al. eds.), *Immunochemical Methods In Cell And Molecular Biology* (Mayer and Walker, eds., Academic Press, London, 1987); *Handbook Of Experimental Immunology*, Volumes I-IV (D. M. Weir and C. C. Blackwell, eds., 1986); *Manipulating the Mouse Embryo*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986).

Brief Description of the Figures

Figure 1 is the atomic coordinates for Arg-5 through Met-147 of SEQ ID No. 2 in standard Brookhaven protein databank (pdb) format.

Figure 2 is a stick figure illustrating the residues of the active site of hUbCE.

Figure 3 is the atomic coordinates for Cys-85, Leu-86, Asp-87, Ile-88, Arg-90, Ser-91, Leu-109, Asn-114, Asp-116, and Asp-117 of SEQ ID No. 2 in standard Brookhaven protein databank (pdb) format.

Figure 5 is a sequence alignment of hUbCE ("human"), spUbCE ("S pombe") and caUbCE ("C albicans").

Figure 4 is the schematic overview of the operation of the GROW method of drug design. The site and seed coordinate file and command file are provided to the GROW procedure by the user. Growth can be visualized as a tree process in which each library template is attached to the seed (A) and then evaluated by the scoring function (e.g. binding criteria). Of the resulting constructs, a given number of best constructs (e.g. 10) are kept for the next level (B). To each retained monopeptide/seed construct are attached all library templates, which are again scored (C). After pruning(D), the process is repeated (E) until the specified peptide length is reached (F). In this tree diagram, circles represent those nodes selected (based on best binding criteria evaluation) for further growth. Uncircled nodes are pruned. Horizontal dots denote continuation across all template additions (e.g. other members of a series), and vertical dots represent the iterative process of tree growth.

Figure 6 illustrate the hUbCE dependent ubiquitination of p53 in an *in vitro* ubiquitination reaction. A complete ubiquitination reaction shown in lane 6 contained E1, hUbCE, E6, E6AP, p53 and ubiquitin. The following changes were made in lanes 1-5: lane 1 no E6, lane 2 no E6AP, lane 3 UBC2 replaces hUbCE, lane 4 no E1, lane 5 no ubiquitin. In lane 7 mutant hUbCE (Cys85→Ser) replaces wild-type hUbCE.

Figure 7A shows the ubiquitination of E6AP. Purified proteins were used in ubiquitination reactions containing biotinylated ubiquitin. Lane 1 ubiquitin, lane 2 E1, ubiquitin and hUbCE, lane 3 E1, ubiquitin, hUbCE and E6AP, lane 4 E1, ubiquitin, hUbCE, E6AP and E6, lane 5 E1, hUbCE, E6AP and E6, lane 6 ubiquitin, hUbCE and E6AP, lane 7 E1, ubiquitin and E6AP, lane 8 ubiquitin and E6AP.

Figure 7B demonstrates the hUbCE-specific ubiquitination of E6AP. All lanes contained E1 and ubiquitin with the following additions: lane 1 nothing, lane 2 hUbCE, lane

3 hUbCE and E6AP, lane 4 GST.UBC8, lane 5 GST.UBC8 and E6AP, lane 6 GST.UBC2, lane 7 GST.UBC2 and E6AP, lane 8 GST.epiUBC, lane 9 GST.epiUBC and E6AP.

Figure 8 shows the degree of inhibition of E6 stimulated p53 degradation in co-injection experiments. The indicated DNAs were co-injected with pX.E6. The levels of inhibition of the E6 stimulated p53 degradation are derived from an analysis of approx. 150 injected cells per experimental point in at least two independent experiments.

Figure 9 depicts am exemplary luciferase reporter construct derived from the pGL2-Basic vector (Promega catalog no. E1641) by addition, in the multiple cloning region, of a SalI to BamHI fragment containing the TK promoter sequence with either 3 or 6 tandemly arranged binding sites (either p53, myc or sP1 binding sites) placed upstream of the TK promoter.

Detailed Description of the Invention

The ubiquitin system is essential for a wide spectrum of cellular phenomena, and is a component of many biological regulatory mechanisms, including aspects of growth control, metabolic regulation, tissue differentiation and development, and cell-cycle progression.

The present invention relates to the discovery of ubiquitin-conjugating enzymes (UBC's) involved in regulating cell cycle progression.

One aspect of the present invention relates to the discovery of a family of related ubiquitin-conjugating enzymes ("UbCE"). In particular, members of this family have been cloned from various eukaryotic sources, and include, for example, a human ubiquitin-conjugating enzyme ("hUbCE"), a *C. albican* ubiquitin-conjugating enzyme ("caUbCE"), and an *S. pombe* ubiquitin-conjugating enzyme ("spUbCE"). The nucleotide sequences for the human UbCE, the *C. albican* UbCE, and the *S. pombe* UbCE coding sequences are provided in SEQ ID Nos. 1, 3 and 5, respectively. The corresponding amino acid sequences are represented in SEQ ID Nos. 2, 4 and 6.

Another aspect of the invention relates to the discovery of a novel human ubiquitin-conjugating enzyme ("rapUBC"). rapUBC has been cloned based on its ability to bind FKBP/rapamycin complexes. The human rapUBC coding sequence is provided in SEQ ID No:12. The corresponding amino acid sequence is represented in SEQ ID No:13.

The biological activity of the UBCE (e.g., UbCE and rapUBC) proteins of the present invention is evidently to be important in a number of basic cellular functions, such as regulation of gene expression, regulation of the cell-cycle, modification of cell surface receptors, biogenesis of ribosomes, and DNA repair. An apparent function of these enzymes in ubiquitin-mediated systems is to control the cellular half-lives of vasrious proteins. For instance, as demonstrated in the Examples, hUbCE is implicated in the ubiquitin-mediated inactivation of cell-cycle regulatory proteins, particularly p53. As is generally known, p53 is a checkpoint protein that plays an important role in sensing DNA damage or regulating

cellular response to stress. Moreover, lesions in the p53 gene have been shown to be associated with a wide variety of proliferative diseases. Consequently, the present invention identifies a potential molecular target, e.g., hUbCE, for regulating the cellular half-life of p53 and thereby modulating, for instance, cell proliferation, apoptosis and cellular sensitivity to chemotherapeutics and DNA damaging agents.

Accordingly, the present invention makes available diagnostic and therapeutic assays, reagents and kits for detecting and treating proliferative disorders arising from, for example, tumorogenic transformation of cells, or other hyperplastic or neoplastic transformation processes. For example, the present invention makes available reagents, such as antibodies and nucleic acid probes, for detecting altered complex formation, and/or altered levels of hUbCE or rapUBC expression, and/or hUbCE or rapUBC-gene deletion or mutation, in order to identify transformed cells. Moreover, the present invention provides a method of treating a wide variety of pathological cell proliferative conditions, such as by gene therapy utilizing recombinant gene constructs encoding the subject UBC proteins, by providing peptidomimetics which either inhibit or potentiate the interaction between the UBC and other cellular proteins, or by providing inhibitors of the catalytic activity of the enzyme. Such methods can also be used in cell and tissue culture, such as to regulate the transformation of cells *in vitro*.

In similar fashion, the present invention also makes available diagnostic and therapeutic assays for detecting and treating yeast/fungal infections, where such infections occur in an animal, e.g. humans, or on a non-living object, such as food or medical instruments. For example, given the apparent role of the subject UbCEs, namely caUbCE and spUbCE, in regulation of proteins involved in growth, mating and proliferation of yeast, inhibitors of the subject ubiquitin conjugating enzyme can be used to treat mycotic infections, as disinfectants, or as food preservatives.

For convenience, certain terms employed in the specification, examples, and appended claims are collected here.

As used herein, the term "nucleic acid" refers to polynucleotides such as deoxyribonucleic acid (DNA), and, where appropriate, ribonucleic acid (RNA). The term should also be understood to include, as equivalents, analogs of either RNA or DNA made from nucleotide analogs, and, as applicable to the embodiment being described, single (sense or antisense) and double-stranded polynucleotides.

As used herein, the terms "gene", "recombinant gene" and "gene construct" refer to a nucleic acid comprising an open reading frame encoding a UBC polypeptide of the present invention, including both exon and (optionally) intron sequences. In preferred embodiments, the nucleic acid is DNA or RNA. Exemplary recombinant genes include nucleic acids which encode all or a catalytically active portion of the hUbCE protein represented in SEQ ID No. 2, the caUbCE protein represented in SEQ ID No. 4, the spUbCE protein represented in SEQ

ID No. 6, or the rapUBC protein represented in SEQ ID No:13. The term "intron" refers to a DNA sequence present in a given UBC-gene which is not translated into protein and is generally found between exons.

The term "transfection" refers to the introduction of a nucleic acid, e.g., an expression vector, into a recipient cell by nucleic acid-mediated gene transfer. "Transformation", as used herein, refers to a process in which a cell's genotype is changed as a result of the cellular uptake of exogenous nucleic acid, and, for example, the transformed cell expresses a recombinant form of one of the subject UBC proteins.

"Cells" or "cell cultures" or "recombinant host cells" or "host cells" are often used interchangeably as will be clear from the context. These terms include the immediate subject cell which expresses a ubiquitin-conjugating enzyme of the present invention, and, of course, the progeny thereof. It is understood that not all progeny are exactly identical to the parental cell, due to chance mutations or difference in environment. However, such altered progeny are included in these terms, so long as the progeny retain the characteristics relevant to those conferred on the originally transformed cell. In the present case, such a characteristic might be the ability to produce a recombinant UBC-protein.

As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. The term "expression vector" includes plasmids, cosmids or phages capable of synthesizing the subject proteins encoded by their respective recombinant genes carried by the vector. Preferred vectors are those capable of autonomous replication and/expression of nucleic acids to which they are linked. In the present specification, "plasmid" and "vector" are used interchangeably as the plasmid is the most commonly used form of vector. Moreover, the invention is intended to include such other forms of expression vectors which serve equivalent functions and which become known in the art subsequently hereto.

"Transcriptional regulatory sequence" is a generic term used throughout the specification to refer to DNA sequences, such as initiation signals, enhancers, and promoters, as well as polyadenylation sites, which induce or control transcription of protein coding sequences with which they are operably linked. In preferred embodiments, transcription of a recombinant UBC-gene is under the control of a promoter sequence (or other transcriptional regulatory sequence) which controls the expression of the recombinant gene in a cell-type in which expression is intended. It will also be understood that the recombinant gene can be under the control of transcriptional regulatory sequences which are the same or which are different from those sequences which control transcription of the naturally-occurring form of the regulatory protein.

The term "tissue-specific promoter" means a DNA sequence that serves as a promoter, i.e., regulates expression of a selected DNA sequence operably linked to the promoter, and which effects expression of the selected DNA sequence in specific cells of a

tissue, such as cells of an epithelial lineage, e.g. cervical squamous cells. In an illustrative embodiment of epithelial-specific promoters, gene constructs can be used as a part of gene therapy to deliver, for example, genes encoding a domaint negative hUbCE or rapUBC mutant, in order to inhibit degradation of p53 required for the pathogenesis of certain papillomavirus-mediated disorders, e.g. papillomas, or to direct expression of an antisense construct of the subject ubiquitin-conjugating enzyme in only epithelial tissue. The term also covers so-called "leaky" promoters, which regulate expression of a selected DNA primarily in one tissue, but cause expression in other tissues as well.

As used herein, a "transgenic animal" is any animal, preferably a non-human mammal in which one or more of the cells of the animal contain heterologous nucleic acid introduced by way of human intervention, such as by trangenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or *in vitro* fertilization, but rather is directed to the introduction of a recombinant DNA molecule. This molecule may be integrated within a chromosome, or it may be extrachromosomally replicating DNA. In the typical transgenic animals described herein, the transgene causes cells to express a recombinant form of the subject UBC protein, e.g. either agonistic or antagonistic forms, or in which the endogenous UBC gene has been disrupted. However, transgenic animals in which the recombinant UBC gene is silent are also contemplated, as for example, the FLP or CRE recombinase dependent constructs described below. The "non-human animals" of the invention include vertebrates such as rodents, non-human primates, sheep, dog, cow, amphibians, reptiles, etc. Preferred non-human animals are selected from the rodent family including rat and mouse, most preferably mouse. The term "chimeric animal" is used herein to refer to animals in which the recombinant gene is found, or in which the recombinant is expressed in some but not all cells of the animal. The term "tissue-specific chimeric animal" indicates that the recombinant UBC gene is present and/or expressed in some tissues but not others.

As used herein, the term "transgene" means a nucleic acid sequence (encoding, e.g., a UBC polypeptide), which is partly or entirely heterologous, i.e., foreign, to the transgenic animal or cell into which it is introduced, or, is homologous to an endogenous gene of the transgenic animal or cell into which it is introduced, but which is designed to be inserted, or is inserted, into the animal's genome in such a way as to alter the genome of the cell into which it is inserted (e.g., it is inserted at a location which differs from that of the natural gene or its insertion results in a knockout). A transgene can include one or more transcriptional regulatory sequences and any other nucleic acid, such as introns, that may be necessary for optimal expression of a selected nucleic acid.

"Homology" refers to sequence similarity between two peptides or between two nucleic acid molecules. Homology can be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When a position in the compared sequence is occupied by the same base or amino acid, then the molecules are homologous at that position. A degree of homology between sequences is a function of the number of matching or homologous positions shared by the sequences.

The term "evolutionarily related to", with respect to nucleic acid sequences encoding the subject ubiquitin-conjugating enzymes, refers to nucleic acid sequences which have arisen naturally in an organism, including naturally occurring mutants. The term also refers to nucleic acid sequences which, while derived from a naturally occurring enzymes, have been altered by mutagenesis, as for example, combinatorial mutagenesis described below, yet still encode polypeptides which have at least one activity of a UBC protein.

As described below, one aspect of this invention pertains to an isolated nucleic acid comprising a nucleotide sequence encoding one of the subject UBC proteins, fragments thereof encoding polypeptides having at least one biological activity of the UBC protein, and/or equivalents of such nucleic acids. The term "nucleic acid" as used herein is intended to include such fragments and equivalents. The term "equivalent" is understood to include nucleotide sequences encoding functionally equivalent UBC proteins or functionally equivalent peptides having an activity of a ubiquitin-conjugating enzyme such as described herein. Equivalent nucleotide sequences will include sequences that differ by one or more nucleotide substitutions, additions or deletions, such as allelic variants; and will also include sequences that differ from the nucleotide sequence encoding the hUbCE gene shown in SEQ ID No: 1, the caUbCE gene shown in SEQ ID No: 3, the spUbCE gene shown in SEQ ID No: 5, or the rapUBC gene shown in SEQ ID No:12, due to the degeneracy of the genetic code. Equivalents will also include nucleotide sequences which hybridize under stringent conditions (i.e., equivalent to about 20-27°C below the melting temperature (T_m) of the DNA duplex formed in about 1M salt) to the nucleotide sequence represented in at least one of SEQ ID Nos: 1, 3, 5 or 12. In one embodiment, equivalents will further include nucleic acid sequences derived from and evolutionarily related to the nucleotide sequences shown in any of SEQ ID Nos: 1, 3, 5 or 12.

The term "isolated" as also used herein with respect to nucleic acids, such as DNA or RNA, refers to molecules separated from other DNAs, or RNAs, respectively, that are present in the natural source of the macromolecule. For example, an isolated nucleic acid encoding on of the subject UBC-proteins preferably includes no more than 10 kilobases (kb) of nucleic acid sequence which naturally immediately flanks the UBC gene in genomic DNA, more preferably no more than 5kb of such naturally occurring flanking sequences, and most preferably less than 1.5kb of such naturally occurring flanking sequence. The term isolated as used herein also refers to a nucleic acid or peptide that is substantially free of cellular

material or culture medium when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. Moreover, an "isolated nucleic acid" is meant to include nucleic acid fragments which are not naturally occurring as fragments and would not be found in the natural state.

Polypeptides referred to herein as possessing the acitivity of a ubiquitin-conjugating enzyme (UBC), e.g. are UBC agonists, are understood to have an amino acid sequence identical to or homologous with the amino acid sequences shown in any on of SEQ ID Nos: 2, 4, 6 or 13, and which are capable of forming a thiol ester adduct with the C-terminal carboxyl group of ubiquitin and transferring the ubiquitin to an ε-amino group in an acceptor protein by formation of an isopeptide bond. The biological activity of the subject UBC proteins can include participation in degradative pathways for selective proteolysis of constitutively or conditionally short-lived proteins as well as abnormal proteins. Antagonistic forms of the subject UBC proteins are defined as proteins that are homologous, but not identical, to the UBC proteins represented in SEQ ID Nos: 2, 4, 6 or 13, or that are fragments of the wild-type proteins, which inhibit the transfer of ubiquitin by the naturally occurring form of the ubiquitin-conjugating enzyme. For instance, as described below, mutations in the active site of the enzyme, e.g. Cys-85, can produce dominant negative forms of the subject UbCEs which antagonize the action of the wild-type form of the protein.

Polypeptides referred to in particular as having an activity of an hUbCE protein are defined as peptides that have an amino acid sequence corresponding to all or a portion of the amino acid sequence of the human ubiquitin conjugating enzyme shown in SEQ ID No: 2 and which have at least one biological activity of an hUbCE protein: such as an ability to mediate ubiquitination of cellular proteins, e.g. cell-cycle regulatory proteins, e.g. p53; an ability to mediate ubiquitin-dependent degradation of cellular proteins, e.g. cell-cycle regulatory proteins, e.g. p53; an ability to affect the cellular half-life of a cell-cycle regulatory protein, e.g. a cell-cycle checkpoint protein, e.g. p53, e.g. in normal cells, e.g. in normal proliferating cells, e.g. in virally-infected cells, e.g. in papillomavirus infected cells, e.g. in HPV-infected cells, e.g. in HPV-16, HPV-18, HPV-31, or HPV-33 infected cells, e.g. in cells expressing a papillomavirus E6 protein, e.g. in transformed cells, e.g. in cancerous cells. Other biological activities of the subject hUbCE proteins are described herein or will be reasonably apparent to those skilled in the art.

Polypeptides referred to in particular as having an activity of a rapUBC protein are defined as peptides that have an amino acid sequence corresponding to all or a portion of the amino acid sequence of the human ubiquitin conjugating enzyme shown in SEQ ID No:13 and which have at least one biological activity of a rapUBC protein: such as an ability to bind a FKBP/rapamycin complex, an ability to mediate ubiquitination of cellular proteins, e.g. cell-cycle regulatory proteins, e.g. p53; an ability to mediate ubiquitin-dependent degradation of cellular proteins, e.g. cell-cycle regulatory proteins, e.g. p53; an ability to

affect the cellular half-life of a cell-cycle regulatory protein, e.g. a cell-cycle checkpoint protein, e.g. p53, e.g. in normal cells, e.g. in cancerous cells. Given that rapamycin causes a block in the cell-cycle during G1 phase, the spectrum of biological activity of the subject rapUBC enzyme is believed to include control of half-lives of certain cell cycle regulatory proteins, particularly relatively short lived proteins (e.g. proteins which have half-lives on the order of 30 minutes to 2 hours). For example, the subject rapUBC may mediate ubiquitination of, for example, p53, myc, p27 and/or cyclins, and therefore affects the cellular half-life of a cell-cycle regulatory protein in proliferating cells. The binding of the rapUBC to the FKBP/rapamycin complex may result in sequestering of the enzyme away from its substrate proteins. Thus, rapamycin may intefere with the ubiquitin-mediated degradation of p53 in a manner which causes cellular p53 levels to rise which in turn inhibits progression of the G1 phase.

Moreover, it will be generally appreciated that, under certain circumstances, it will be advantageous to provide homologs of naturally-occurring forms of the subject UBC proteins which are either agonists or antagonists of only a subset of that protein's biological activities. Thus, specific biological effects can be elicited by treatment with a homolog of limited function, and with fewer side effects relative to treatment with agonists or antagonists which are directed to all of the biological activities of that protein. For example, hUbCE and rapUBC homologs can be generated which bind to and inhibit activation of other proteins in the ubiquitin pathway of p53 without substantially interfering with the ubiquitination of other cellular proteins.

In one embodiment, the nucleic acid of the invention encodes a polypeptide which is either an agonist or antagonist the human UBC protein and comprises an amino acid sequence represented by SEQ ID No: 2. Preferred nucleic acids encode a peptide having an hUbCE protein activity, or which is an antagonist thereof, and being at least 90% homologous, more preferably 95% homologous and most preferably 97% homologous with an amino acid sequence shown in SEQ ID No: 2. Nucleic acids which encode agonist or antagonist forms of an hUbCE protein and having at least about 98-99% homology with a sequence shown in SEQ ID No: 2 are also within the scope of the invention. Preferably, the nucleic acid is a cDNA molecule comprising at least a portion of the nucleotide sequence encoding an hUbCE protein shown in SEQ ID No. 1. A preferred portion of the cDNA molecule shown in SEQ ID No. 1 includes the coding region of the molecule.

In another embodiment, the nucleic acid of the invention encodes a polypeptide which is either an agonist or antagonist a *Candida* UbCE protein, e.g. a *C. albican* UbCE, and comprises an amino acid sequence represented by SEQ ID No: 4. Preferred nucleic acids encode a peptide having an caUbCE protein activity, or which is an antagonist thereof, and being at least 90% homologous, more preferably 95% homologous and most preferably 97% homologous with an amino acid sequence shown in SEQ ID No: 4. Nucleic acids which

encode agonist or antagonist forms of an caUbCE protein and having at least about 98-99% homology with a sequence shown in SEQ ID No: 4 are also within the scope of the invention. Preferably, the nucleic acid is a cDNA molecule comprising at least a portion of the nucleotide sequence encoding an caUbCE protein shown in SEQ ID No. 3. A preferred portion of the cDNA molecule shown in SEQ ID No. 3 includes the coding region of the molecule. The present invention contemplates closely related homologs (orthologs) from other species of *Candida*, e.g. *Candida stellatoidea*, *Candida tropicalis*, *Candida parapsilosis*, *Candida krusei*, *Candida pseudotropicalis*, *Candida quillermondii*, or *Candida rugosa*.

In yet another embodiment, the nucleic acid of the invention encodes a polypeptide which is either an agonist or antagonist of a *Schizosaccharomyces* UbCE protein, e.g. an *S. pombe* UbCE, and comprises an amino acid sequence represented by SEQ ID No: 6. Preferred nucleic acids encode a peptide having an spUbCE protein activity, or which is an antagonist thereof, and being at least 90% homologous, more preferably 95% homologous and most preferably 97% homologous with an amino acid sequence shown in SEQ ID No: 6. Nucleic acids which encode agonist or antagonist forms of an spUbCE protein and having at least about 98-99% homology with a sequence shown in SEQ ID No: 6 are also within the scope of the invention. Preferably, the nucleic acid is a cDNA molecule comprising at least a portion of the nucleotide sequence encoding an spUbCE protein shown in SEQ ID No. 5. A preferred portion of the cDNA molecule shown in SEQ ID No. 5 includes the coding region of the molecule.

In yet another embodiment, the nucleic acid of the invention encodes a polypeptide which is either an agonist or antagonist of the human UBC protein and comprises an amino acid sequence represented by SEQ ID No:13. Preferred nucleic acids encode a peptide having a rapUBC protein activity, or which is an antagonist thereof, and being at least 90% homologous, more preferably 95% homologous and most preferably 97% homologous with an amino acid sequence shown in SEQ ID No:13. Nucleic acids which encode agonist or antagonist forms of a rapUBC protein and having at least about 98-99% homology with a sequence shown in SEQ ID No:13 are also within the scope of the invention. Preferably, the nucleic acid is a cDNA molecule comprising at least a portion of the nucleotide sequence encoding a rapUBC protein shown in SEQ ID No:12. A preferred portion of the cDNA molecule shown in SEQ ID No:12 includes the coding region of the molecule.

Another aspect of the invention provides a nucleic acid which hybridizes under high or low stringency conditions to a nucleic acid which encodes a peptide having all or a portion of an amino acid sequence shown in one of SEQ ID Nos: 2, 4, 6 or 13. Appropriate stringency conditions which promote DNA hybridization, for example, 6.0 x sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0 x SSC at 50°C, are known to those skilled in the art or can be found in *Current Protocols in Molecular Biology*,

John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. For example, the salt concentration in the wash step can be selected from a low stringency of about 2.0 x SSC at 50°C to a high stringency of about 0.2 x SSC at 50°C. In addition, the temperature in the wash step can be increased from low stringency conditions at room temperature, about 22°C, to high stringency conditions at about 65°C.

Isolated nucleic acids which differ in sequence from the nucleotide sequences represented in SEQ ID Nos: 1, 3, 5 or 12 due to degeneracy in the genetic code are also within the scope of the invention. Such nucleic acids can encode functionally equivalent peptides (i.e., a peptide having a biological activity of a UBC protein) but differ in sequence from the sequence shown in SEQ ID No: 1, 3, 5 or 12 due to degeneracy in the genetic code. For example, a number of amino acids are designated by more than one triplet. Codons that specify the same amino acid, or synonyms (for example, CAU and CAC are synonyms for histidine) may result in "silent" mutations which do not affect the amino acid sequence of the subject UBC protein. However, it is expected that DNA sequence polymorphisms that do lead to changes in the amino acid sequences of the present hUbCE or rapUBC proteins will exist from one human subject to the next. One skilled in the art will appreciate that these variations in one or more nucleotides (up to about 3-4% of the nucleotides) of the nucleic acids encoding peptides having an activity of, for example, an hUbCE or a rapUBC protein may exist among individuals due to natural allelic variation. Any and all such nucleotide variations and resulting amino acid polymorphisms are within the scope of this invention.

Fragments of the nucleic acid encoding an active portion of one of the subject ubiquitin-conjugating enzymes are also within the scope of the invention. As used herein, a fragment of the nucleic acid encoding an active portion of a UBC protein refers to a nucleotide sequence having fewer nucleotides than the nucleotide sequence encoding the entire amino acid sequence of the protein but which encodes a peptide which possess agonistic or antagonistic activity relative to a naturally occurring form of the enzyme.

Nucleic acid fragments within the scope of the invention also include those capable of hybridizing under high or low stringency conditions with nucleic acids from other species for use in screening protocols to detect UBC homologs.

Nucleic acids within the scope of the invention may also contain linker sequences, modified restriction endonuclease sites and other sequences useful for molecular cloning, expression or purification of recombinant peptides having at least one biological activity of the subject UbCE ubiquitin-conjugating enzymes. In a preferred embodiment, the nucleic acid fragment comprises at least a portion of the nucleic acid sequence represented by nucleotide residues 319 through 441 of SEQ ID No. 1, corresponding to amino acid residues Cys-107 through Met-147. In preferred embodiments, the nucleic acid encodes an hUbCE polypeptide which includes Cys-107 through Cys-111, and more preferably includes Cys-107 through Asp-117. As illustrated by Figure 2, certain of the residues from Cys-107 to Asp-

111 are important members of the ubiquitin-binding site of hUbCE. Correspondingly, nucleic acid encoding caUbCE or spUbCE preferably include Cys-107 through Val-147 and Cys-107 through Ile-107, respectively.

As indicated by the examples set out below, a nucleic acid encoding a peptide having an activity of the subject ubiquitin-conjugating enzymes may be obtained from mRNA or genomic DNA present in any of a number of eukaryotic cells in accordance with protocols described herein, as well as those generally known in the art. A cDNA encoding a homolog of one of the human UBC proteins, for example, can be obtained by isolating total mRNA from a cell, e.g. a mammalian cell. Double stranded cDNAs can then be prepared from the total mRNA, and subsequently inserted into a suitable plasmid or bacteriophage vector using any one of a number of known techniques. A gene encoding a UBC protein can also be cloned using established polymerase chain reaction techniques in accordance with the nucleotide sequence information provided herein.

Another aspect of the invention relates to the use of the isolated nucleic acid in "antisense" therapy. As used herein, "antisense" therapy refers to administration or *in situ* generation of oligonucleotide probes or their derivatives which specifically hybridizes (e.g. binds) under cellular conditions, with the cellular mRNA and/or genomic DNA encoding a UBC protein so as to inhibit expression of that protein, e.g. by inhibiting transcription and/or translation. The binding may be by conventional base pair complementarity, or, for example, in the case of binding to DNA duplexes, through specific interactions in the major groove of the double helix. In general, "antisense" therapy refers to the range of techniques generally employed in the art, and includes any therapy which relies on specific binding to oligonucleotide sequences.

An antisense construct of the present invention can be delivered, for example, as an expression plasmid which, when transcribed in the cell, produces RNA which is complementary to at least a unique portion of the cellular mRNA which encodes one of the subject UBC-proteins, e.g. the human hUbCE gene represented in SEQ ID No. 1 or the rapUBC gene represented in SEQ ID No:12. Alternatively, the antisense construct can be an oligonucleotide probe which is generated *ex vivo* and which, when introduced into the cell causes inhibition of expression by hybridizing with the mRNA and/or genomic sequences encoding one of the UBC proteins. Such oligonucleotide probes are preferably modified oligonucleotide which are resistant to endogenous nucleases, e.g. exonucleases and/or endonucleases, and are therefore stable *in vivo*. Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphothioate and methylphosphonate analogs of DNA (see also U.S. Patents 5,176,996; 5,264,564; and 5,256,775). Additionally, general approaches to constructing oligomers useful in antisense therapy have been reviewed, for example, by van der Krol et al. (1988) *Biotechniques* 6:958-976; and Stein et al. (1988) *Cancer Res* 48:2659-2668.

Accordingly, the modified oligomers of the invention are useful in therapeutic, diagnostic, and research contexts. In therapeutic applications, the oligomers are utilized in a manner appropriate for antisense therapy in general. For such therapy, the oligomers of the invention can be formulated for a variety of loads of administration, including systemic and topical or localized administration. Techniques and formulations generally may be found in Remmington's Pharmaceutical Sciences, Meade Publishing Co., Easton, PA. For systemic administration, injection is preferred, including intramuscular, intravenous, intraperitoneal, and subcutaneuos for injection, the oligomers of the invention can be formulated in liquid solutions, preferably in physiologically compatible buffers such as Hank's solution or Ringer's solution. In addition, the oligomers may be formulated in solid form and redissolved or suspended immediately prior to use. Lyophilized forms are also included.

Systemic administration can also be by transmucosal or transdermal means, or the compounds can be administered orally. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration bile salts and fusidic acid derivatives. In addition, detergents may be used to facilitate permeation. Transmucosal administration may be through nasal sprays or using suppositories. For oral administration, the oligomers are formulated into conventional oral administration forms such as capsules, tablets, and tonics. For topical administration, the oligomers of the invention are formulated into ointments, salves, gels, or creams as generally known in the art.

In addition to use in therapy, the oligomers of the invention may be used as diagnostic reagents to detect the presence or absence of the target DNA or RNA sequences to which they specifically bind. Such diagnostic tests are described in further detail below.

This invention also provides expression vectors containing a nucleic acid encoding the subject UBC proteins, operably linked to at least one transcriptional regulatory sequence. Operably linked is intended to mean that the nucleic acid is linked to a transcriptional regulatory sequence in a manner which allows expression of the enzyme encoded by the nucleic acid, and that expression is, for example, either constitutively or inducibly controlled by the transcriptional regulatory sequence. Regulatory sequences are art-recognized. Accordingly, the term regulatory sequence includes promoters, enhancers and other expression control elements. Such regulatory sequences are described in Goeddel; *Gene Expression Technology*: *Methods in Enzymology* 185, Academic Press, San Diego, CA (1990).

For instance, any of a wide variety of expression control sequences-sequences that control the expression of a DNA sequence when operatively linked to it may be used in these vectors to express DNA sequences encoding the UBC proteins of this invention. Such useful expression control sequences, include, for example, the early and late promoters of SV40,

adenovirus or cytomegalovirus immediate early promoter, the lac system, the trp system, the TAC or TRC system, T7 promoter whose expression is directed by T7 RNA polymerase, the major operator and promoter regions of phage lambda, the control regions for fd coat protein, the promoter for 3-phosphoglycerate kinase or other glycolytic enzymes, the promoters of acid phosphatase, e.g., Pho5, the promoters of the yeast alpha -mating factors, the polyhedron promoter of the baculovirus system and other sequences known to control the expression of genes of prokaryotic or eukaryotic cells or their viruses, and various combinations thereof. It should be understood that the design of the expression vector may depend on such factors as the choice of the host cell to be transformed and/or the type of protein desired to be expressed. Moreover, the vector's copy number, the ability to control that copy number and the expression of any other proteins encoded by the vector, such as antibiotic markers, should also be considered.

In one embodiment, the expression vector includes DNA encoding one of the subject hUbCE proteins, e.g. a recombinant hUbCE protein. Similar expression vectors for producing recombinant forms of the rapUBC protein are also contemplated. Such expression vectors can be used to transfect cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein.

Moreover, hUbCE or rapUBC-expression vectors can be used as a part of a gene therapy protocol to reconstitute hUbCE or rapUBC function in a mammalian cell in which hUbCE or rapUBC is misexpressed, or alternatively, to provide an antagonist of the naturally-occurring hUbCE or rapUBC, or an antisense construct -such as to inhibit hUbCE or rapUBC-mediated degradation of a cell-cycle regulatory protein For instance, expression constructs of the subject hUbCE or rapUBC-proteins may be administered in any biologically effective carrier, e.g. any formulation or composition capable of effectively transfecting cells *in vivo* with a recombinant hUbCE or rapUBC-gene. Approaches include insertion of the subject gene in viral vectors including recombinant retroviruses, adenovirus, adeno-associated virus, and herpes simplex virus-1, or recombinant bacterial or eukaryotic plasmids. Viral vectors can be used to transfect cells directly; plasmid DNA can be delivered with the help of, for example, cationic liposomes (lipofectin) or derivatized (e.g. antibody conjugated), polylysine conjugates, gramacidin S, artificial viral envelopes or other such intracellular carriers, as well as direct injection of the gene construct or $CaPO_4$ precipitation carried out *in vivo*. It will be appreciated that because transduction of appropriate target cells represents the critical first step in gene therapy, choice of the particular gene delivery system will depend on such factors as the phenotype of the intended target and the route of administration, e.g. locally or systemically.

A preferred approach for *in vivo* introduction of nucleic acid encoding one of the subject proteins into a cell is by use of a viral vector containing nucleic acid, e.g. a cDNA, encoding the gene product. Infection of cells with a viral vector has the advantage that a

large proportion of the targeted cells can receive the nucleic acid. Additionally, molecules encoded within the viral vector, e.g., by a cDNA contained in the viral vector, are expressed efficiently in cells which have taken up viral vector nucleic acid.

Retrovirus vectors and adeno-associated virus vectors are generally understood to be the recombinant gene delivery system of choice for the transfer of exogenous genes *in vivo*, particularly into humans. These vectors provide efficient delivery of genes into cells, and the transferred nucleic acids are stably integrated into the chromosomal DNA of the host. A major prerequisite for the use of retroviruses is to ensure the safety of their use, particularly with regard to the possibility of the spread of wild-type virus in the cell population. The development of specialized cell lines (termed "packaging cells") which produce only replication-defective retroviruses has increased the utility of retroviruses for gene therapy, and defective retroviruses are well characterized for use in gene transfer for gene therapy purposes (for a review see Miller, A.D. (1990) *Blood* 76:271). Thus, recombinant retrovirus can be constructed in which part of the retroviral coding sequence (*gag, pol, env*) has been replaced by nucleic acid encoding one of the subject hUbCE or rapUBC-proteins rendering the retrovirus replication defective. The replication defective retrovirus is then packaged into virions which can be used to infect a target cell through the use of a helper virus by standard techniques. Protocols for producing recombinant retroviruses and for infecting cells *in vitro* or *in vivo* with such viruses can be found in Current Protocols in Molecular Biology, Ausubel, F.M. et al. (eds.) Greene Publishing Associates, (1989), Sections 9.10-9.14 and other standard laboratory manuals. Examples of suitable retroviruses include pLJ, pZIP, pWE and pEM which are well known to those skilled in the art. Examples of suitable packaging virus lines for preparing both ecotropic and amphotropic retroviral systems include ψCrip, ψCre, ψ2 and ψAm. Retroviruses have been used to introduce a variety of genes into many different cell types, including neural cells, epithelial cells, endothelial cells, lymphocytes, myoblasts, hepatocytes, bone marrow cells, *in vitro* and/or *in vivo* (see for example Eglitis, et al. (1985) *Science* 230:1395-1398; Danos and Mulligan (1988) *Proc. Natl. Acad. Sci. USA* 85:6460-6464; Wilson et al. (1988) *Proc. Natl. Acad. Sci. USA* 85:3014-3018; Armentano et al. (1990) *Proc. Natl. Acad. Sci. USA* 87:6141-6145; Huber et al. (1991) *Proc. Natl. Acad. Sci. USA* 88:8039-8043; Ferry et al. (1991) *Proc. Natl. Acad. Sci. USA* 88:8377-8381; Chowdhury et al. (1991) *Science* 254:1802-1805; van Beusechem et al. (1992) *Proc. Natl. Acad. Sci. USA* 89:7640-7644; Kay et al. (1992) *Human Gene Therapy* 3:641-647; Dai et al. (1992) *Proc. Natl. Acad. Sci. USA* 89:10892-10895; Hwu et al. (1993) *J. Immunol.* 150:4104-4115; U.S. Patent No. 4,868,116; U.S. Patent No. 4,980,286; PCT Application WO 89/07136; PCT Application WO 89/02468; PCT Application WO 89/05345; and PCT Application WO 92/07573).

Furthermore, it has also been shown that it is possible to limit the infection spectrum of retroviruses and consequently of retroviral-based vectors, by modifying the viral

packaging proteins on the surface of the viral particle (see, for example PCT publications WO93/25234, WO94/06920, and WO94/11524). For instance, strategies for the modification of the infection spectrum of retroviral vectors include: coupling antibodies specific for cell surface antigens to the viral *env* protein (Roux et al. (1989) *PNAS* 86:9079-9083; Julan et al. (1992) *J. Gen Virol* 73:3251-3255; and Goud et al. (1983) *Virology* 163:251-254); or coupling cell surface ligands to the viral *env* proteins (Neda et al. (1991) *J Biol Chem* 266:14143-14146). Coupling can be in the form of the chemical cross-linking with a protein or other variety (e.g. lactose to convert the *env* protein to an asialoglycoprotein), as well as by generating fusion proteins (e.g. single-chain antibody/*env* fusion proteins). This technique, while useful to limit or otherwise direct the infection to certain tissue types, and can also be used to convert an ecotropic vector in to an amphotropic vector.

Moreover, use of retroviral gene delivery can be further enhanced by the use of tissue- or cell-specific transcriptional regulatory sequences which control expression of the hUbCE or rapUBC-gene of the retroviral vector.

Another viral gene delivery system useful in the present invention utilitizes adenovirus-derived vectors. The genome of an adenovirus can be manipulated such that it encodes a gene product of interest, but is inactivate in terms of its ability to replicate in a normal lytic viral life cycle (see, for example, Berkner et al. (1988) *BioTechniques* 6:616; Rosenfeld et al. (1991) *Science* 252:431-434; and Rosenfeld et al. (1992) *Cell* 68:143-155). Suitable adenoviral vectors derived from the adenovirus strain Ad type 5 dl324 or other strains of adenovirus (e.g., Ad2, Ad3, Ad7 etc.) are well known to those skilled in the art. Recombinant adenoviruses can be advantageous in certain circumstances in that they are not capable of infecting nondividing cells and can be used to infect a wide variety of cell types, including airway epithelium (Rosenfeld et al. (1992) cited *supra*), endothelial cells (Lemarchand et al. (1992) *Proc. Natl. Acad. Sci. USA* 89:6482-6486), hepatocytes (Herz and Gerard (1993) *Proc. Natl. Acad. Sci. USA* 90:2812-2816) and muscle cells (Quantin et al. (1992) *Proc. Natl. Acad. Sci. USA* 89:2581-2584). Furthermore, the virus particle is relatively stable and amenable to purification and concentration, and as above, can be modified so as to affect the spectrum of infectivity. Additionally, introduced adenoviral DNA (and foreign DNA contained therein) is not integrated into the genome of a host cell but remains episomal, thereby avoiding potential problems that can occur as a result of insertional mutagenesis in situations where introduced DNA becomes integrated into the host genome (e.g., retroviral DNA). Moreover, the carrying capacity of the adenoviral genome for foreign DNA is large (up to 8 kilobases) relative to other gene delivery vectors (Berkner et al., *supra*; Haj-Ahmand and Graham (1986) *J. Virol.* 57:267). Most replication-defective adenoviral vectors currently in use and therefore favored by the present invention are deleted for all or parts of the viral E1 and E3 genes but retain as much as 80% of the adenoviral

genetic material (see, e.g., Jones et al. (1979) *Cell* 16:683; Berkner et al., *supra*; and Graham et al. in Methods in Molecular Biology, E.J. Murray, Ed. (Humana, Clifton, NJ, 1991) vol. 7. pp. 109-127). Expression of the inserted hUbCE or rapUBC-gene can be under control of, for example, the E1A promoter, the major late promoter (MLP) and associated leader sequences, the E3 promoter, or exogenously added promoter sequences.

Yet another viral vector system useful for delivery of the subject hUbCE or rapUBC-genes is the adeno-associated virus (AAV). Adeno-associated virus is a naturally occurring defective virus that requires another virus, such as an adenovirus or a herpes virus, as a helper virus for efficient replication and a productive life cycle. (For a review see Muzyczka et al. *Curr. Topics in Micro. and Immunol.* (1992) 158:97-129). It is also one of the few viruses that may integrate its DNA into non-dividing cells, and exhibits a high frequency of stable integration (see for example Flotte et al. (1992) *Am. J. Respir. Cell. Mol. Biol.* 7:349-356; Samulski et al. (1989) *J. Virol.* 63:3822-3828; and McLaughlin et al. (1989) *J. Virol.* 62:1963-1973). Vectors containing as little as 300 base pairs of AAV can be packaged and can integrate. Space for exogenous DNA is limited to about 4.5 kb. An AAV vector such as that described in Tratschin et al. (1985) *Mol. Cell. Biol.* 5:3251-3260 can be used to introduce DNA into cells. A variety of nucleic acids have been introduced into different cell types using AAV vectors (see for example Hermonat et al. (1984) *Proc. Natl. Acad. Sci. USA* 81:6466-6470; Tratschin et al. (1985) *Mol. Cell. Biol.* 4:2072-2081; Wondisford et al. (1988) *Mol. Endocrinol.* 2:32-39; Tratschin et al. (1984) *J. Virol.* 51:611-619; and Flotte et al. (1993) *J. Biol. Chem.* 268:3781-3790).

Other viral vector systems that may have application in gene therapy have been derived from herpes virus, vaccinia virus, and several RNA viruses. In particular, herpes virus vectors may provide a unique strategy for persistence of the recombinant hUbCE or rapUBC-genes in cells of the central nervous system and occular tissue (Pepose et al. (1994) Invest Ophthalmol Vis Sci 35:2662-2666).

In addition to viral transfer methods, such as those illustrated above, non-viral methods can also be employed to cause expression of an hUbCE or rapUBC-protein, or an hUbCE or a rapUBC antisense molecule, in the tissue of an animal. Most nonviral methods of gene transfer rely on normal mechanisms used by mammalian cells for the uptake and intracellular transport of macromolecules. In preferred embodiments, non-viral gene delivery systems of the present invention rely on endocytic pathways for the uptake of the subject hUbCE or rapUBC-gene by the targeted cell. Exemplary gene delivery systems of this type include liposomal derived systems, poly-lysine conjugates, and artificial viral envelopes.

In a representative embodiment, a gene encoding one of the subject ubiquitin-conjugating enzymes can be entrapped in liposomes bearing positive charges on their surface (e.g., lipofectins) and (optionally) which are tagged with antibodies against cell surface antigens of the target tissue (Mizuno et al. (1992) *No Shinkei Geka* 20:547-551; PCT

publication WO91/06309; Japanese patent application 1047381; and European patent publication EP-A-43075). For example, lipofection of papilloma-virus infected epithelial cells can be carried out using liposomes tagged with monoclonal antibodies against, for example, squamous cells.

In similar fashion, the gene delivery system comprises an antibody or cell surface ligand which is cross-linked with a gene binding agent such as poly-lysine (see, for example, PCT publications WO93/04701, WO92/22635, WO92/20316, WO92/19749, and WO92/06180). For example, the subject UBC-gene construct can be used to transfect HPV-infected squamous cells *in vivo* using a soluble polynucleotide carrier comprising an HPV viral caot protein conjugated to a polycation, e.g. poly-lysine (see U.S. Patent 5,166,320). It will also be appreciated that effective delivery of the subject nucleic acid constructs via -mediated endocytosis can be improved using agents which enhance escape of the gene from the endosomal structures. For instance, whole adenovirus or fusogenic peptides of the influenza HA gene product can be used as part of the delivery system to induce efficient disruption of DNA-containing endosomes (Mulligan et al. (1993) *Science* 260-926; Wagner et al. (1992) *PNAS* 89:7934; and Christiano et al. (1993) PNAS 90:2122).

In clinical settings, the gene delivery systems can be introduced into a patient by any of a number of methods, each of which is familiar in the art. For instance, a pharmaceutical preparation of the gene delivery system can be introduced systemically, e.g. by intravenous injection, and specific transduction of the in the target cells occurs predominantly from specificity of transfection provided by the gene delivery vehicle, cell-type or tissue-type expression due to the transcriptional regulatory sequences controlling expression of the gene, or a combination thereof. In other embodiments, initial delivery of the recombinant gene is more limited with introduction into the animal being quite localized. For example, the gene delivery vehicle can be introduced by catheter (see U.S. Patent 5,328,470) or by stereotactic injection (e.g. Chen et al. (1994) *PNAS* 91: 3054-3057).

Moreover, the pharmaceutical preparation can consist essentially of the gene delivery system in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery system can be produced intact from recombinant cells, e.g. retroviral packages, the pharmaceutical preparation can comprise one or more cells which produce the gene delivery system. In the case of the latter, methods of introducing the viral packaging cells may be provided by, for example, rechargeable or biodegradable devices. The generation of such implants is generally known in the art. See, for example, *Concise Encyclopedia of Medical & Dental Materials*, ed. by David Williams (MIT Press: Cambridge, MA, 1990); Sabel et al. U.S. Patent No. 4,883,666; Aebischer et al. U.S. Patent No. 4,892,538; Aebischer et al. U.S. Patent No. 5,106,627; Lim U.S. Patent No. 4,391,909; Sefton U.S. Patent No. 4,353,888; and Aebischer et al. (1991) *Biomaterials* 12:50-55).

This invention also pertains to a host cell transfected or transformed to express a recombinant forms of the subject UBC proteins. The host cell may be any prokaryotic or eukaryotic cell. For example, an hUbCE or rapUBC polypeptide of the present invention may be expressed in bacterial cells such as *E. coli*, insect cells (baculovirus), yeast, or mammalian cells. Other suitable host cells are known to those skilled in the art.

The term "recombinant protein" refers to a protein of the present invention which is produced by recombinant DNA techniques, wherein generally DNA encoding the UBC protein is inserted into a suitable expression vector which is in turn used to transform a host cell to produce the heterologous protein. Moreover, the phrase "derived from", with respect to a recombinant gene encoding the recombinant UBC, is meant to include within the meaning of "recombinant protein" those proteins having an amino acid sequence of a native UBC, e.g. hUbCE, caUbCE, spUbCE, or rapUBC, or an amino acid sequence similar thereto which is generated by mutations including substitutions and deletions of a naturally occurring form of the protein. Recombinant proteins preferred by the present invention, in addition to native proteins, are at least 90% homologous, more preferably 95% homologous and most preferably 97% homologous with an amino acid sequence shown in one of SEQ ID Nos: 2, 4, 6 or 13. Polypeptides having an activity of a UBC protein, or which are antagonistic thereto, and which are at least about 90%, more preferably at least about 95%, and most preferably at least about 98-99% homologous with a sequence shown in SEQ ID No: 2, 4, 6 or 13 are also within the scope of the invention.

The present invention further pertains to recombinant UBC homologs which are encoded by genes derived from other non-human mammals, e.g. mouse, rat, rabbit, or pig, and which have amino acid sequences evolutionarily related to an hUbCE or rapUBC protein. As described above, such recombinant UBC or rapUBC proteins preferably are capable of functioning in one of either role of an agonist or antagonist of at least one biological activity of an hUbCE or rapUBC. The term "evolutionarily related to", as set out above, refers to ubiquitin-conjugating enzymes having amino acid sequences which have arisen naturally, or which are mutationally derived, for example, by combinatorial mutagenesis or scanning mutagenesis, but which proteins are homologous to either the hUbCE protein represented in SEQ ID No: 2 or rapUBC protein represented in SEQ ID No:13.

The present invention further pertains to methods of producing the subject proteins. For example, a host cell transfected with an expression vector encoding one of the subject UBC proteins can be cultured under appropriate conditions to allow expression of the polypeptide to occur. The peptide may be secreted (e.g. through use of recombinantly added signal sequence) and isolated from a mixture of cells and medium containing the secreted protein. Alternatively, the peptide may be retained cytoplasmically, as it presumably is its naturally occurring form, and the cells harvested, lysed and the protein isolated. A cell culture includes host cells, media and other byproducts. Suitable media for cell culture are

well known in the art. The subject UBC polypeptides can be isolated from cell culture medium, host cells, or both using techniques known in the art for purifying proteins including ion-exchange chromatography, gel filtration chromatography, ultrafiltration, electrophoresis, and immunoaffinity purification with antibodies raised against the protein. In a preferred embodiment, the UBC protein is a fusion protein containing a domain which facilitates its purification, such as the hUbCE-GST fusion protein described below.

Thus, a nucleotide sequence derived from the cloning of a UBC protein of the present invention, encoding all or a selected portion of the protein, can be used to produce a recombinant form of the enzyme via microbial or eukaryotic cellular processes. Ligating the polynucleotide sequence into a gene construct, such as an expression vector, and transforming or transfecting into hosts, either eukaryotic (yeast, avian, insect or mammalian) or prokaryotic (bacterial cells), are standard procedures used in producing other well-known proteins, e.g. p53, C-myc, cyclins, cdks and the like. Similar procedures, or modifications thereof, can be employed to prepare recombinant proteins, or portions thereof, by microbial means or tissue-culture technology in accord with the subject invention.

The recombinant protein can be produced by ligating the cloned gene, or a portion thereof, into a vector suitable for expression in either prokaryotic cells, eukaryotic cells, or both. Expression vehicles for production of recombinant UBCs include plasmids and other vectors. For instance, suitable vectors for the expression of the subject proteins include plasmids of the types: pBR322-derived plasmids, pEMBL-derived plasmids, pEX-derived plasmids, pBTac-derived plasmids and pUC-derived plasmids for expression in prokaryotic cells, such as *E. coli*.

A number of vectors exist for the expression of recombinant proteins in yeast. For instance, YEP24, YIP5, YEP51, YEP52, pYES2, and YRP17 are cloning and expression vehicles useful in the introduction of genetic constructs into *S. cerevisiae* (see, for example, Broach et al. (1983) in *Experimental Manipulation of Gene Expression*, ed. M. Inouye Academic Press, p. 83, incorporated by reference herein). These vectors can replicate in *E. coli* due the presence of the pBR322 ori, and in *S. cerevisiae* due to the replication determinant of the yeast 2 micron plasmid. In addition, drug resistance markers such as ampicillin can be used.

The preferred mammalian expression vectors contain both prokaryotic sequences to facilitate the propagation of the vector in bacteria, and one or more eukaryotic transcription units that are expressed in eukaryotic cells. The pcDNAI/amp, pcDNAI/neo, pRc/CMV, pSV2gpt, pSV2neo, pSV2-dhfr, pTk2, pRSVneo, pMSG, pSVT7, pko-neo and pHyg derived vectors are examples of mammalian expression vectors suitable for transfection of eukaryotic cells. Some of these vectors are modified with sequences from bacterial plasmids, such as pBR322, to facilitate replication and drug resistance selection in both prokaryotic and eukaryotic cells. Alternatively, derivatives of viruses such as the bovine papilloma virus

(BPV-1), or Epstein-Barr virus (pHEBo, pREP-derived and p205) can be used for transient expression of proteins in eukaryotic cells. The various methods employed in the preparation of the plasmids and transformation of host organisms are well known in the art. For other suitable expression systems for both prokaryotic and eukaryotic cells, as well as general recombinant procedures, see *Molecular Cloning: A Laboratory Manual*, 2nd Ed., ed. by Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory Press:1989) Chapters 16 and 17.

In some instances, it may be desirable to express the recombinant UBc by the use of a baculovirus expression system. Examples of such baculovirus expression systems include pVL-derived vectors (such as pVL1392, pVL1393 and pVL941), pAcUW-derived vectors (such as pAcUW1), and pBlueBac-derived vectors (such as the ß-gal containing pBlueBac III).

When expression of a portion of the ubiquitin-conjugating enzyme is desired, i.e. a truncation mutant, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from *E. coli* (Ben-Bassat et al. (1987) *J. Bacteriol.* 169:751-757) and *Salmonella typhimurium* and its *in vitro* activity has been demonstrated on recombinant proteins (Miller et al. (1987) *PNAS* 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either *in vivo* by expressing UBC-derived polypeptides in a host which produces MAP (e.g., *E. coli* or CM89 or *S. cerevisiae*), or *in vitro* by use of purified MAP (e.g., procedure of Miller et al.).

Alternatively, the coding sequences for the polypeptide can be incorporated as a part of a fusion gene including a nucleotide sequence encoding a different polypeptide. This type of expression system can be useful under conditions where it is desirable to produce an immunogenic fragment of a UBC protein. In an exemplary embodiment, the VP6 capsid protein of rotavirus can be used as an immunologic carrier protein for portions of the hUbCE or rapUBC polypeptide, either in the monomeric form or in the form of a viral particle. The nucleic acid sequences corresponding to the portion of the hUbCE or rapUBC protein to which antibodies are to be raised can be incorporated into a fusion gene construct which includes coding sequences for a late vaccinia virus structural protein to produce a set of recombinant viruses expressing fusion proteins comprising a portion of the protein hUbCE or rapUBC as part of the virion. It has been demonstrated with the use of immunogenic fusion proteins utilizing the Hepatitis B surface antigen fusion proteins that recombinant Hepatitis B virions can be utilized in this role as well. Similarly, chimeric constructs coding for fusion proteins containing a portion of an UBC protein and the poliovirus capsid protein can be created to enhance immunogenicity of the set of polypeptide antigens (see, for example, EP

Publication No. 0259149; and Evans et al. (1989) *Nature* 339:385; Huang et al. (1988) *J. Virol.* 62:3855; and Schlienger et al. (1992) *J. Virol.* 66:2).

The Multiple Antigen Peptide system for peptide-based immunization can also be utilized, wherein a desired portion of a UBC protein is obtained directly from organo-chemical synthesis of the peptide onto an oligomeric branching lysine core (see, for example, Posnett et al. (1988) *J Biol Chem* 263:1719 and Nardelli et al. (1992) *J. Immunol.* 148:914). Antigenic determinants of the UBC proteins can also be expressed and presented by bacterial cells.

In addition to utilizing fusion proteins to enhance immunogenicity, it is widely appreciated that fusion proteins can also facilitate the expression of proteins, such as the UBC proteins of the present invention. For example, as described below, the hUbCE protein can be generated as a glutathione-S-transferase (GST) fusion protein. Such GST fusion proteins can enable purification of the hUbCE protein, such as by the use of glutathione-derivatized matrices (see, for example, *Current Protocols in Molecular Biology,* eds. Ausubel et al. (NY: John Wiley & Sons, 1991); Smith et al. (1988) *Gene* 67:31; and Kaelin et al. (1992) *Cell* 70:351). In another embodiment, a fusion gene coding for a purification leader sequence, such as a poly-(His)/enterokinase cleavage site sequence at the N-terminus of the desired portion of the hUbCE protein, can allow purification of the expressed hUbCE -fusion protein by affinity chromatography using a Ni^{2+} metal resin. The purification leader sequence can then be subsequently removed by treatment with enterokinase (e.g., see Hochuli et al. (1987) *J. Chromatography* 411:177; and Janknecht et al. *PNAS* 88:8972). Similar constructs can be generated for expression of rapUBC, caUbCE, or spUbCE.

Techniques for making fusion genes are well known. Essentially, the joining of various DNA fragments coding for different polypeptide sequences is performed in accordance with conventional techniques, employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausabel et al. John Wiley & Sons: 1992).

Various modifications of the hUbCE protein to produce these and other functionally equivalent peptides are described in detail herein. In similar fashion, homologs of the subject rapUBC, caUBC and spUBC polypeptides are contemplated, including both agonistic and antagonistic forms. The term peptide, as used herein, refers to peptides, proteins, and polypeptides.

The present invention also makes available isolated UBC proteins, which proteins are isolated from or otherwise substantially free of other extracellular proteins, especially other proteins of the ubiquitin conjugating system (i.e. other E1 or E2 enzymes, as well as E3 proteins or ubiquitin) normally associated with the ubiquitin-conjugating enzyme in the cellular milleau. The term "substantially free of other extracellular proteins" (also referred to herein as "contaminating proteins") is defined as encompassing preparations of the subject UBC protein comprising less than 20% (by dry weight) contaminating protein, and preferably comprising less than 5% contaminating protein. Functional forms of the subject UBC proteins can be prepared, for the first time, as purified preparations by using a cloned gene as described herein. By "purified", it is meant, when referring to a peptide or DNA or RNA sequence, that the indicated molecule is present in the substantial absence of other biological macromolecules, such as other proteins (particularly other enzymes of the ubiquitin system such as other E1 or E2 proteins, as well as other contaminating proteins). The term "purified" as used herein preferably means at least 80% by dry weight, more preferably in the range of 95-99% by weight, and most preferably at least 99.8% by weight, of biological macromolecules of the same type present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 5000, can be present). The term "pure" as used herein preferably has the same numerical limits as "purified" immediately above. "Isolated" and "purified" do not encompass either natural materials in their native state or natural materials that have been separated into components (e.g., in an acrylamide gel) but not obtained either as pure (e.g. lacking contaminating proteins or chromatography reagents such as denaturing agents and polymers, e.g. acrylamide or agarose) substances or solutions.

Isolated peptides having an activity of an UBC protein, or which can function as antagonists of a naturally occurring form of the UBC protein described herein can also be obtained by screening peptides recombinantly produced from the corresponding fragment of the nucleic acids encoding such peptides. In addition, fragments can be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry. For example, the hUbCE protein may be arbitrarily divided into fragments of desired length with no overlap of the fragments, or preferably divided into overlapping fragments of a desired length. The fragments can be produced (recombinantly or by chemical synthesis) and tested to identify those peptides having an hUbCE protein activity or alternatively to identify antagonists. Similar manipulation of the rapUBC, caUbCE and soUbCE proteins can be carried out.

Furthermore, it is also possible to modify the structure of a UBC polypeptide for such purposes as enhancing therapeutic or prophylactic efficacy, or stability (e.g., shelf life *ex vivo* and resistance to proteolytic degradation *in vivo*). Such modified peptides are considered functional equivalents of peptides having an activity of, or which antagonize, a UBC protein

as defined herein. A modified polypeptide can be produced in which the amino acid sequence has been altered, such as by amino acid substitution, deletion, or addition.

For example, it is reasonable to expect that an isolated replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, a threonine with a serine, or a similar replacement of an amino acid with a structurally related amino acid (i.e. conservative mutations) will not have a major effect on the biological activity of the resulting molecule. Conservative replacements are those that take place within a family of amino acids that are related in their side chains. Genetically encoded amino acids are can be divided into four families: (1) acidic = aspartate, glutamate; (2) basic = lysine, arginine, histidine; (3) nonpolar = alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan; and (4) uncharged polar = glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine. Phenylalanine, tryptophan, and tyrosine are sometimes classified jointly as aromatic amino acids. In similar fashion, the amino acid repertoire can be grouped as (1) acidic = aspartate, glutamate; (2) basic = lysine, arginine histidine, (3) aliphatic = glycine, alanine, valine, leucine, isoleucine, serine, threonine, with serine and threonine optionally be grouped separately as aliphatic-hydroxyl; (4) aromatic = phenylalanine, tyrosine, tryptophan; (5) amide = asparagine, glutamine; and (6) sulfur -containing = cysteine and methionine. (see, for example, *Biochemistry*, 2nd ed, Ed. by L. Stryer, WH Freeman and Co.:1981). Whether a change in the amino acid sequence of a peptide results in a functional UBC homolog can be readily determined by assessing the ability of the variant peptide to, for instance, mediate ubiquitination in a fashion similar to the wild-type UBC. Peptides in which more than one replacement has taken place can readily be tested in the same manner.

The invention also includes a method of generating sets of combinatorial mutants of the subject UBC proteins, as well as truncation and fragmentation mutants, and is especially useful for identifying potential variant sequences which are functional in ubiquitinating cellular proteins. One purpose for screening such combinatorial libraries is, for example, to isolate novel UBC homologs which act as antagonist of the wild-type ("authentic") UBC activity, e.g. an hUbCE homolog which inhibits p53 ubiquitination, or alternatively, possess novel activities all together. Such proteins, when expressed from recombinant DNA constructs, can be used in gene therapy protocols.

Likewise, mutagenesis can give rise to UBC homologs which have intracellular half-lives dramatically different than the corresponding wild-type protein. For example, the altered protein can be rendered either more stable or less stable to proteolytic degradation or other cellular process which result in destruction of, or otherwise inactivation of, a naturally occurring form of the subject hUbCE or rapUBC proteins. Such hUbCE or rapUBC homologs (either agonist or antagonist homologs), and the genes which encode them, can be utilized to alter the envelope of recombinant hUbCE or rapUBC expression by modulating the half-life of the protein. For instance, a short half-life for the recombinant hUbCE or

rapUBC can give rise to more transient biological effects associated with that homolog and, when part of an inducible expression system, can allow tighter control of recombinant hUbCE or rapUBC levels within the cell. As above, such proteins, and particularly their recombinant nucleic acid constructs, can be used in gene therapy protocols.

In one aspect of this method, the amino acid sequences for a population of UBC homologs or other related proteins are aligned, preferably to promote the highest homology possible. Such a population of variants can include, for example, hUbCE or rapUBC homologs from one or more species, or UBC homologs from the same species but which differ due to mutation. Amino acids which appear at each position of the aligned sequences are selected to create a degenerate set of combinatorial sequences. For instance, alignment of the hUbCE, caUbCE and spUbCE sequences provided in the appended sequence listing (see also Figure 5) can be used to generate a degenerate library of UbCE proteins represented by the general formula:

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Met-Xaa(1)-Leu-Lys-Arg-Ile-Xaa(2)-Xaa(3)-Glu-Leu-
Xaa(4)-Asp-Leu-Xaa(5)-Xaa(6)-Asp-Pro-Pro-Xaa(7)-
Xaa(8)-Cys-Ser-Ala-Gly-Pro-Val-Gly-Asp-Asp-Xaa(9)-
Xaa(10)-His-Trp-Gln-Ala-Xaa(11)-Ile-Met-Gly-Pro-Asn-
Asp-Ser-Pro-Tyr-Xaa(12)-Gly-Gly-Val-Phe-Phe-Leu-
Xaa(13)-Ile-His-Phe-Pro-Thr-Asp-Tyr-Pro-Xaa(14)-Lys-
Pro-Pro-Lys-Xaa(15)-Xaa(16)-Xaa(17)-Thr-Thr-Xaa(18)-
Ile-Tyr-His-Pro-Asn-Ile-Asn-Ser-Asn-Gly-Xaa(19)-Ile-
Cys-Leu-Asp-Ile-Leu-Xaa(20)-Xaa(21)-Gln-Trp-Ser-Pro-
Ala-Leu-Thr-Ile-Ser-Lys-Val-Leu-Leu-Ser-Ile-Cys-Ser-
Leu-Leu-Xaa(22)-Asp-Xaa(23)-Asn-Pro-Asp-Asp-Pro-Leu-
Val-Pro-Glu-Ile-Ala-Xaa(24)-Xaa(25)-Tyr-Xaa(26)-
Xaa(27)-Asp-Arg-Xaa(28)-Xaa(29)-Tyr-Xaa(30)-Xaa(31)-
Xaa(32)-Ala-Xaa(33)-Glu-Trp-Thr-Xaa(34)-Lys-Tyr-Ala-
Xaa(35)                                    (SEQ ID No. 7)
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wherein Xaa(1) represents Ala or Ser; Xaa(2) represents His or Asn; Xaa(3) represents Lys or Arg; Xaa(4) represents Ala, Ser or Asn; Xaa(5) represents Gly or Ala; Xaa(6) represents Arg or Lys; Xaa(7) represents Ala or Ser; Xaa(8) represents Gln or Ser; Xaa(9) represents Leu or Met; Xaa(10) represents Phe or Tyr; Xaa(11) represents Ser or Thr; Xaa(12) represents Gln or Ala; Xaa(13) represents Ser or Thr; Xaa(14) represents Leu or Phe; Xaa(15) represents Val or Ile; Xaa(16) represents Ala or Asn; Xaa(17) represents Leu or Phe; Xaa(18) represents Arg or Lys; Xaa(19) represents Ser or Asn; Xaa(20) represents Arg or Lys; Xaa(21) represents Ser or Asp; Xaa(22) represents Thr or Cys; Xaa(23) represents Ala or Pro; Xaa(24) represents Arg or His; Xaa(25) represents Val or Ile; Xaa(26) represents Lys or Gln; Xaa(27) represents Thr or Gln; Xaa(28) represents Ser, Lys or Glu; Xaa(29) represents Arg or Lys; Xaa(30) represents Asn or Gln; Xaa(31) represents Ala, Leu or Arg; Xaa(32) represents Ile, Ser or

Thr; Xaa(33) represents Arg or Lys; Xaa(34) represents Arg, Lys or Gln; Xaa(35) represents Val, Ile or Met.

To further expand the library, each of the degenerate positions (Xaa) can be rendered even more degenerate by including other amino acid residues which are of the same "family" as the residues which appear in each of the UbCEs, e.g. Xaa(1) can be Gly, Ala, Val, Leu, Ile, Ser or Thr (e.g. aliphatic), Xaa(22) can be Ser, Thr, Cys or Met (aliphatic-hydroxyl and sulfur-containing), etc.. Alternatively, isosteric substitutions can be made without regard to, for example, charge or polarity of the amino acid sidechain. For instance, Xaa(17) can be Leu, Ile, Asn, Met, Phe or Tyr, as the sidechains of Ile, Asn and Met each occupy approximately the same steric space as Leu, and Tyr is isosteric for Phe. Likewise, where the degeneracy is conserved from the human and yeast homologs, the degenerate libarary can, at that position, only include, for example, the amino acid residue which occurs in the human UbCE. To illustrate, Xaa(3) is a Lysine in hUbCE and caUbCE, and Arginine in spUbCE. In a library which rejects conservative mutations of the human UbCE as equivalent, Xaa(3) would be Lys.

In a preferred embodiment, the combinatorial UBC library is produced by way of a degenerate library of genes encoding a library of polypeptides which each include at least a portion of potential UBC sequences. A mixture of synthetic oligonucleotides can be enzymatically ligated into gene sequences such that the degenerate set of potential UBC sequences are expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g. for phage display) containing the set of UBC sequences therein.

There are many ways by which the library of potential UBC homologs can be generated from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be carried out in an automatic DNA synthesizer, and the synthetic genes then be ligated into an appropriate gene for expression. The purpose of a degenerate set of genes is to provide, in one mixture, all of the sequences encoding the desired set of potential UBC sequences. The synthesis of degenerate oligonucleotides is well known in the art (see, for example, Narang, SA (1983) *Tetrahedron* 39:3; Itakura et al. (1981) *Recombinant DNA, Proc 3rd Cleveland Sympos. Macromolecules*, ed. AG Walton, Amsterdam: Elsevier pp273-289; Itakura et al. (1984) *Annu. Rev. Biochem.* 53:323; Itakura et al. (1984) *Science* 198:1056; Ike et al. (1983) *Nucleic Acid Res.* 11:477. Such techniques have been employed in the directed evolution of other proteins (see, for example, Scott et al. (1990) *Science* 249:386-390; Roberts et al. (1992) *PNAS* 89:2429-2433; Devlin et al. (1990) *Science* 249: 404-406; Cwirla et al. (1990) *PNAS* 87: 6378-6382; as well as U.S. Patents Nos. 5,223,409, 5,198,346, and 5,096,815).

A wide range of techniques are known in the art for screening gene products of combinatorial libraries made by point mutations, and for screening cDNA libraries for gene products having a certain property. Such techniques will be generally adaptable for rapid

screening of the gene libraries generated by the combinatorial mutagenesis of UBC homologs. The most widely used techniques for screening large gene libraries typically comprises cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates relatively easy isolation of the vector encoding the gene whose product was detected. Each of the illustrative assays described below are amenable to high through-put analysis as necessary to screen large numbers of, for example, degenerate UBC sequences created by combinatorial mutagenesis techniques.

In one illustrative screening assay, the candidate hUbCE or rapUBC gene products are displayed on the surface of a cell or viral particle, and the ability of particular cells or viral particles to bind other components of the ubiquitin pathway, such as E1 or E3 proteins (e.g. E6AP or E6AP complexes), ubiquitin, or a cell-cycle regulatory protein, via this gene product is detected in a "panning assay". For instance, the gene library can be cloned into the gene for a surface membrane protein of a bacterial cell, and the resulting fusion protein detected by panning (Ladner et al., WO 88/06630; Fuchs et al. (1991) *Bio/Technology* 9:1370-1371; and Goward et al. (1992) *TIBS* 18:136-140). In a similar fashion, fluorescently labeled molecules which bind hUbCE or rapUBC can be used to score for potentially functional hUbCE or rapUBC homologs. Cells can be visually inspected and separated under a fluorescence microscope, or, where the morphology of the cell permits, separated by a fluorescence-activated cell sorter.

In an alternate embodiment, the gene library is expressed as a fusion protein on the surface of a viral particle. For instance, in the filamentous phage system, foreign peptide sequences can be expressed on the surface of infectious phage, thereby conferring two significant benefits. First, since these phage can be applied to affinity matrices at very high concentrations, a large number of phage can be screened at one time. Second, since each infectious phage displays the combinatorial gene product on its surface, if a particular phage is recovered from an affinity matrix in low yield, the phage can be amplified by another round of infection. The group of almost identical *E.coli* filamentous phages M13, fd, and f1 are most often used in phage display libraries, as either of the phage gIII or gVIII coat proteins can be used to generate fusion proteins without disrupting the ultimate packaging of the viral particle (Ladner et al. PCT publication WO 90/02909; Garrard et al., PCT publication WO 92/09690; Marks et al. (1992) *J. Biol. Chem.* 267:16007-16010; Griffiths et al. (1993) *EMBO J* 12:725-734; Clackson et al. (1991) *Nature* 352:624-628; and Barbas et al. (1992) *PNAS* 89:4457-4461).

In an illustrative embodiment, the recombinant phage antibody system (RPAS, Pharmacia Catalog number 27-9400-01) can be easily modified for use in expressing and screening hUbCE or rapUBC combinatorial libraries. For instance, the pCANTAB 5

phagemid of the RPAS kit contains the gene which encodes the phage gIII coat protein. The hUbCE or rapUBC combinatorial gene library can be cloned into the phagemid adjacent to the gIII signal sequence such that it will be expressed as a gIII fusion protein. After ligation, the phagemid is used to transform competent *E. coli* TG1 cells. Transformed cells are subsequently infected with M13KO7 helper phage to rescue the phagemid and its candidate hUbCE or rapUBC gene insert. The resulting recombinant phage contain phagemid DNA encoding a specific candidate hUbCE or rapUBC, and display one or more copies of the corresponding fusion coat protein. The phage-displayed candidate hUbCE or rapUBC which are capable of binding a particular target protein, such as an E1 enzyme, an E3 protein (i.e. E6 or E6-AP), or a particular regulatory protein (such as p53 or p27), are selected or enriched by panning. For instance, the phage library can be panned on glutathione immobilized p53-GST fusion proteins or E6-GST or E6-AP-GST fusion proteins and unbound phage washed away from the cells. The bound phage is then isolated, and if the recombinant phage express at least one copy of the wild type gIII coat protein, they will retain the ability to infect *E. coli*. Thus, successive rounds of reinfection and panning can be employed to greatly enrich for UBC homologs that retain some ability to interact with normal targets of the wild-type enzyme and which can then be screened for further biological activities in order to differentiate agonists and antagonists. In an exemplary embodiment, by use of two or more target proteins in sequential panning steps, the phage display library can be used to isolate hUbCE or rapUBC homologs which are candidate antagonists of the normal cellular function of the naturally occurring UBC . For instance, isolating from the library those variants which retain the ability to bind, for example, either the papillomavirus E6 protein or the cellular E6-AP protein, but which are unable to bind p53, provides a set of hUbCE or rapUBC homologs some of which may be capable of antagonizing the ability of the corresponding wild-type enzyme to mediate ubiquitination of p53.

In yet another illustrative embodiment, the p53-dependent reporter construct described in the 08/176,937 application can be used to identify antagonists through their ability to enhance expression of the reporter gene by inhibiting the degradation of p53 wild-type hUbCE or rapUBC. Thus, a combinatorial library can screened by a detecting expression of the reporter gene, and appropriate clones isolated for further manipulation.

Other forms of mutagenesis can also be utilized to generate a combinatorial library from the subject UBC proteins. For example, hUbCE or rapUBC homologs (both agonist and antagonist forms) can be generated and isolated from a library by screening using, for example, alanine scanning mutagenesis and the like (Ruf et al. (1994) *Biochemistry* 33:1565-1572; Wang et al. (1994) *J. Biol. Chem.* 269:3095-3099; Balint et al. (1993) *Gene* 137:109-118; Grodberg et al. (1993) *Eur. J. Biochem.* 218:597-601; Nagashima et al. (1993) *J. Biol. Chem.* 268:2888-2892; Lowman et al. (1991) *Biochemistry* 30:10832-10838; and Cunningham et al. (1989) *Science* 244:1081-1085), by linker scanning mutagenesis (Gustin et

al. (1993) *Virology* 193:653-660; Brown et al. (1992) *Mol. Cell Biol.* 12:2644-2652; McKnight et al. (1982) *Science* 232:316); by saturation mutagenesis (Meyers et al. (1986) *Science* 232:613); by PCR mutagenesis (Leung et al. (1989) *Method Cell Mol Biol* 1:11-19); or by random mutagenesis (Miller et al. (1992) *A Short Course in Bacterial Genetics*, CSHL Press, Cold Spring Harbor, NY; and Greener et al. (1994) *Strategies in Mol Biol* 7:32-34).

An important goal of the present invention is to provide reduction of the UBC proteins to small functional units that can be ultimately used to generate UBC mimetics, e.g. peptide or non-peptide agents, which are able to disrupt binding of UBC with other cellular and/or viral proteins. Thus, such mutagenic techniques as described herein are particularly useful to map the determinants of the hUbCE or rapUBC protein which participate in protein-protein interactions involved in, for example, binding of the subject hUbCE or rapUBC to other proteins of the ubiquitin-conjugating system (both cellular and viral), as well as the target protein itself (e.g. a cell-cycle regulatory protein). To illustrate, the critical residues of hUbCE involved in molecular recognition of E6 and/or E6-AP can be determined and used to generate hUbCE-derived peptidomimetics which competitively inhibit hUbCE binding. By employing, for example, scanning mutagenesis to map the amino acid residues of hUbCE involved in binding E6AP, peptidomimetic compounds can be generated which mimic those residues in binding to E6AP, and which therefore can inhibit binding of the hUbCE to E6AP and interfere with the function of E6AP in regulating the cellular half-life of p53. For instance, non-hydrolyzable peptide analogs of such residues can be generated using benzodiazepine (e.g., see Freidinger et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), azepine (e.g., see Huffman et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), substituted gama lactam rings (Garvey et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), keto-methylene pseudopeptides (Ewenson et al. (1986) *J Med Chem* 29:295; and Ewenson et al. in *Peptides: Structure and Function* (Proceedings of the 9th American Peptide Symposium) Pierce Chemical Co. Rockland, IL, 1985), β-turn dipeptide cores (Nagai et al. (1985) *Tetrahedron Lett* 26:647; and Sato et al. (1986) *J Chem Soc Perkin Trans* 1:1231), and β-aminoalcohols (Gordon et al. (1985) *Biochem Biophys Res Commun*126:419; and Dann et al. (1986) *Biochem Biophys Res Commun* 134:71). Such peptidomimetics can serve as drugs which prevent the action of hUbCE in the destruction of, for example, p53. Furthermore, such data concerning protein-protein interactions can be used in conjunction with the molecular model of hUbCE described below for rational design of mimetics of this interaction. In like manner, peptidomimetics of caUbCE and spUbCE can be derived which may be useful in, for example, the generation of anti-mycotic agents.

Another aspect of the invention pertains to an antibody specifically reactive with the subject UBC proteins. For example, by using immunogens derived from the hUbCE or

rapUBC protein of the present invention, anti-protein/anti-peptide antisera or monoclonal antibodies can be made by standard protocols (See, for example, *Antibodies: A Laboratory Manual* ed. by Harlow and Lane (Cold Spring Harbor Press: 1988)). A mammal such as a mouse, a hamster or rabbit can be immunized with an immunogenic form of the peptide (e.g., the whole UBC protein or an antigenic fragment which is capable of eliciting an antibody response). Techniques for conferring immunogenicity on a protein or peptide include conjugation to carriers or other techniques well known in the art. An immunogenic portion of the subject UBC protein can be administered in the presence of adjuvant. The progress of immunization can be monitored by detection of antibody titers in plasma or serum. Standard ELISA or other immunoassays can be used with the immunogen as an antigen to assess the levels of antibodies. In a preferred embodiment, the subject antibodies are immunospecific for hUbCE antigenic determinants, e.g. antigenic determinants of a protein represented by SEQ ID No. 2 or a closely related human or non-human mammalian homolog (e.g. 90 percent homologous to SEQ ID No. 2, preferably at least 95 percent homologous and more preferably at least 97 percent homologous to SEQ ID No.2). In yet a further preferred embodiment of the present invention, the anti-hUbCE antibodies does not substantially cross react with a protein which is: e.g. less than 90 percent homologous with SEQ ID No. 2; e.g. less than 95 percent homologous with SEQ ID No. 2; e.g. less than 98-99 percent homologous with SEQ ID No.2. By "does not substantially cross-react", it is meant that: the antibody has a binding affinity for a non-homologous E2 enzyme which is less than 10 percent, more preferably less than 5 percent, and most preferably less than about 1-2 percent of the binding affinity of that antibody for the protein of SEQ ID No. 2; the antibody does not specifically bind a protein which is non-homologous to SEQ ID No. 2. Preferred antibodies against the subject caUbCE, spUbCE and rapUBC proteins have similar criteria, e.g., antibodies specific for caUbCE, spUbCE or rapUBC do not specifically bind proteins which do not share high sequence homology with SEQ ID No. 4, 6, or 13 respectively.

Following immunization, antisera selectively reactive with one or more of the subject UBCs can be obtained and, if desired, polyclonal anti-UBC antibodies isolated from the serum. To produce monoclonal antibodies, antibody producing cells (lymphocytes) can be harvested from an immunized animal and fused by standard somatic cell fusion procedures with immortalizing cells such as myeloma cells to yield hybridoma cells. Such techniques are well known in the art, an include, for example, the hybridoma technique (originally developed by Kohler and Milstein, (1975) *Nature*, 256: 495-497), the human B cell hybridoma technique (Kozbar et al., (1983) *Immunology Today*, 4: 72), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al., (1985) *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc. pp. 77-96). Hybridoma cells can be screened immunochemically for production of antibodies specifically reactive with the

subject proteins and monoclonal antibodies isolated from a culture comprising such hybridoma cells..

The term antibody as used herein is intended to include fragments thereof which are also specifically reactive with the UBC proteins of the present invention. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as described above for whole antibodies. For example, $F(ab')_2$ fragments can be generated by treating antibody with pepsin. The resulting $F(ab')_2$ fragment can be treated to reduce disulfide bridges to produce Fab' fragments. The antibody of the present invention is further intended to include bispecific and chimeric molecules having an anti-UBC portion.

Both monoclonal and polyclonal antibodies (Ab) directed against the subject ubiquitin conjugating enzymes, and antibody fragments such as Fab` and $F(ab`)_2$, can be used as specialty chemicals to block the action of the enzyme and allow the study of, for example, the cell cycle or cell proliferation when the subject UBC is inhibited, e.g. by microinjection of anti-UBC antibodies.

Antibodies which specifically bind hUbCE or rapUBC epitopes can also be used in immunohistochemical staining of tissue samples in order to evaluate the abundance and pattern of expression of hUbCE or rapUBC. Anti-hUbCE or anti-rapUBC antibodies can be used diagnostically in immuno-precipitation and immuno-blotting to detect and evaluate hUbCE or rapUBC levels in tissue or bodily fluid as part of a clinical testing procedure. For instance, such measurements can be useful in predictive valuations of the onset or progression of tumors. Likewise, the ability to monitor hUbCE or rapUBC levels in an individual can allow determination of the efficacy of a given treatment regimen for an individual afflicted with such a disorder. The level of each of the subject UBCs can be measured in cells isolated from bodily fluid, such as in samples of cerebral spinal fluid or blood, or can be measured in tissue, such as produced by biopsy. Diagnostic assays using anti-hUbCE or anti-rapUBC antibodies can include, for example, immunoassays designed to aid in early diagnosis of a neoplastic or hyperplastic disorder, e.g. the presence of cancerous cells in the sample, e.g. to detect cells in which a lesion of the hUbCE or rapUBC gene has occurred.

Another application of anti-UBC antibodies is in the immunological screening of cDNA libraries constructed in expression vectors, such as λgt11, λgt18-23, λZAP, and λORF8. Messenger libraries of this type, having coding sequences inserted in the correct reading frame and orientation, can produce fusion proteins. For instance, λgt11 will produce fusion proteins whose amino termini consist of ß-galactosidase amino acid sequences and whose carboxy termini consist of a foreign polypeptide. Antigenic epitopes of UBc can then be detected with antibodies, as, for example, reacting nitrocellulose filters lifted from infected plates with anti-UBC antibodies. Phage, scored by this assay, can then be isolated from the infected plate. Thus, the presence of hUbCE or rapUBC homologs can be detected and

cloned from other human sources, i.e. to identify other closely homologous human isoforms, as well as to identify hUbCE or rapUBC homologs in other mammals.

Moreover, the nucleotide sequence determined from the cloning of the subject hUbCE or rapUBC from a human cell line will further allow for the generation of probes designed for use in identifying hUbCE or rapUBC homologs in other human cell-types, particularly cancer or other transformed or immortalized cells, as well as hUbCE or rapUBC homologs from other non-human mammals. Probes based on the yeast UbCE sequences, caUbCE and spUbCE, can be generated and used to identify and phenotype mycotic infections.

In addition, nucleotide probes can be generated from the cloned sequence of the hUbCE or rapUBC protein, which allow for histological screening of intact tissue and tissue samples for the presence of hUbCE or rapUBC mRNA. Similar to the diagnostic uses of anti-hUbCE or anti-rapUBC antibodies, the use of probes directed to hUbCE or rapUBC mRNA, or to genomic hUbCE or rapUBC sequences, can be used for both predictive and therapeutic evaluation of allelic mutations which might be manifest in, for example, neoplastic or hyperplastic disorders (e.g. unwanted cell growth). Used in conjunction with anti-hUbCE or anti-rapUBC antibody immunoassays, the nucleotide probes can help facilitate the determination of the molecular basis for a developmental disorder which may involve some abnormality associated with expression (or lack thereof) of an hUbCE or a rapUBC protein. For instance, variation in hUbCE or rapUBC synthesis can be differentiated from a mutation in the hUbCE or rapUBC coding sequence.

For example, the present method provides a method for determining if a subject is at risk for a disorder characterized by unwanted cell proliferation. In preferred embodiments, the subject method can be generally characterized as comprising detecting, in a tissue of a subject (e.g. a human patient), the presence or absence of a genetic lesion characterized by at least one of (i) a mutation of a gene encoding hUbCE or rapUBC, or (ii) the mis-expression of the UBC gene. To illustrate, such genetic lesions can be detected by ascertaining the existence of at least one of (i) a deletion of one or more nucleotides from the UBC gene, (ii) an addition of one or more nucleotides to the UBC gene, (iii) a substitution of one or more nucleotides of the UBC gene, (iv) a gross chromosomal rearrangement of the hUbCE or rapUBC gene, (v) a gross alteration in the level of a messenger RNA transcript of the hUbCE or rapUBC gene, (vi) the presence of a non-wild type splicing pattern of a messenger RNA transcript of the hUbCE or rapUBC gene, and (vii) a non-wild type level of the hUbCE or rapUBC protein. In one aspect of the invention there is provided a probe/primer comprising an oligonucleotide containing a region of nucleotide sequence which is capable of hybridizing to a sense or antisense sequence of SEQ ID No: 1 or SEQ ID No:12, or naturally occurring mutants thereof, or 5' or 3' flanking sequences, or intronic sequences naturally associated with the hUbCE or rapUBC gene. The probe is exposed to nucleic acid of a tissue sample; and the hybridization of the probe to the sample nucleic acid is detected. In certain

embodiments, detection of the lesion comprises utilizing the probe/primer in, for example, a polymerase chain reaction (PCR) (see, e.g., U.S. Patent Nos. 4,683,195 and 4,683,202), or, alternatively, in a ligation chain reaction (LCR) (see, e.g., Landegran et al. (1988) *Science* 241:1077-1080; and Nakazawa et al. (1994) *PNAS* 91:360-364), the later of which can be particularly useful for detecting even point mutations in the hUbCE or rapUBC gene. Alternatively, or additionally, the level of hUbCE or rapUBC protein can be detected in an immunoassay.

Also, the use of anti-sense techniques (e.g. microinjection of antisense molecules, or transfection with plasmids whose transcripts are anti-sense with regard to, e.g. UBC mRNA) can be used to investigate the role of each of the subject UBC proteins in the cell cycle and cell proliferation, by inhibiting endogenous production of that protein. Such techniques can be utilized in cell culture, but can also be used in the creation of transgenic animals.

Another aspect of the present invention concerns transgenic animals, e.g. as animal models for developmental and proliferative diseases, which are comprised of cells (of that animal) which contain a transgene of the present invention and which preferably (though optionally) express a recombinant form (agonist or antagonist) of one or more of the subject UBC enzymes in one or more cells in the animal. In preferred embodiments, the expression of the transgene is restricted to specific subsets of cells, tissues or developmental stages utilizing, for example, cis-acting sequences that control expression in the desired pattern. In the present invention, such mosiac expression of the subject UBC proteins can be essential for many forms of lineage analysis and can additionally provide a means to assess the effects of UBC mutations or overexpression that might grossly alter development in small patches of tissue within an otherwise normal embryo. Toward this and, tissue-specific regulatory sequences and conditional regulatory sequences can be used to control expression of the transgene in certain spatial patterns. Moreover, temporal patterns of expression can be provided by, for example, conditional recombination systems or prokaryotic transcriptional regulatory sequences.

Genetic techniques which allow for the expression of transgenes can be regulated via site-specific genetic manipulation *in vivo* are known to those skilled in the art. For instance, genetic systems are available which allow for the regulated expression of a recombinase that catalyzes the genetic recombination a target sequence. As used herein, the phrase "target sequence" refers to a nucleotide sequence that is genetically recombined by a recombinase. The target sequence is flanked by recombinase recognition sequences and is generally either excised or inverted in cells expressing recombinase activity. Recombinase catalyzed recombination events can be designed such that recombination of the target sequence results in either the activation or repression of expression of the subject receptor. For example, excision of a target sequence which interferes with the expression of the receptor can be designed to activate expression of that protein. This interference with expression of the

subject protein can result from a variety of mechanisms, such as spatial separation of the UBC gene from the promoter element or an internal stop codon. Moreover, the transgene can be made wherein the coding sequence of the UBC gene is flanked by recombinase recognition sequences and is initially transfected into cells in a 3' to 5' orientation with respect to the promoter element. In such an instance, inversion of the target sequence will reorient the subject UBC gene by placing the 5' end of the coding sequence in an orientation with respect to the promoter element which allow for promoter driven transcriptional activation.

In an illustrative embodiment, either the *cre/loxP* recombinase system of bacteriophage P1 (Lakso et al. (1992) *PNAS* 89:6232-6236; Orban et al. (1992) *PNAS* 89:6861-6865) or the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman et al. (1991) *Science* 251:1351-1355; PCT publication WO 92/15694) can be used to generate *in vivo* site-specific genetic recombination systems. Cre recombinase catalyzes the site-specific recombination of an intervening target sequence located between *loxP* sequences. *loxP* sequences are 34 base pair nucleotide repeat sequences to which the Cre recombinase binds and are required for Cre recombinase mediated genetic recombination. The orientation of *loxP* sequences determines whether the intervening target sequence is excised or inverted when Cre recombinase is present (Abremski et al. (1984) *J. Biol. Chem.* 259:1509-1514); catalyzing the excision of the target sequence when the *loxP* sequences are oriented as direct repeats and catalyzes inversion of the target sequence when *loxP* sequences are oriented as inverted repeats.

Accordingly, genetic recombination of the target sequence is dependent on expression of the Cre recombinase. Expression of the recombinase can be regulated by promoter elements which are subject to regulatory control, e.g., tissue-specific, developmental stage-specific, inducible or repressible by externally added agents. This regulated control will result in genetic recombination of the target sequence only in cells where recombinase expression is mediated by the promoter element. Thus, the activation of expression of the recombinant UBC gene can be regulated via regulation of recombinase expression.

Use of the these recombinase system to regulate expression of, for example, a dominant negative UBC gene, such as the Cys85Ser mutant or an antisense gene, requires the construction of a transgenic animal containing transgenes encoding both the Cre recombinase and the subject gene. Animals containing both the Cre recombinase and the UBC genes can be provided through the construction of "double" transgenic animals. A convenient method for providing such animals is to mate two transgenic animals each containing a transgene, e.g., the UBC gene and recombinase gene.

One advantage derived from initially constructing transgenic animals containing a UBC transgene in a recombinase-mediated expressible format derives from the likelihood that the subject UBC protein, whether antagonistic or agonistic, will be deleterious upon

expression in the transgenic animal. In such an instance, a founder population, in which the subject transgene is silent in all tissues, can be propagated and maintained. Individuals of this founder population can be crossed with animals expressing the recombinase in, for example, one or more tissues. Thus, the creation of a founder population in which the UBC transgene is silent will allow the study of, for example, the role of the p53 checkpoint in tissue or at developmental stages which can confer, for example, a lethal phenotype.

Similar conditional transgenes can be provided using prokaryotic promoter sequences which require prokaryotic proteins to be simultaneous expressed in order to facilitate expression of the transgene. Exemplary promoters and the corresponding trans-activating prokaryotic proteins are given in U.S. Patent No. 4,833,080. Moreover, expression of the conditional transgenes can be induced by gene therapy-like methods wherein a gene encoding the trans-activating protein, e.g. a recombinase or a prokaryotic protein, is delivered to the tissue and caused to be expressed, such as in a cell-type specific manner. By this method, the transgene could remain silent into adulthood until "turned on" by the introduction of the trans-activator.

Methods of making knock-out or disruption transgenic animals are also generally known. See, for example, *Manipulating the Mouse Embryo*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986).

Furthermore, the present invention, by making available purified and recombinant forms of the subject UBC proteins, facilitates the development of assays that can be used to screen for drugs which inhibit the conjugating activity. For instance, in addition to agents which disrupt binding of a *UBC* protein to other cellular (or viral) proteins, inhibitors of the enzymatic activity of the subject E2 enzymes may prevent transfer of ubiquitin to the enzyme (by an E1 enzyme) or inhibit any downstream transfer of ubiquitin from the E2 enzyme to a cellular substrate or an intermediary E3 complex, e.g., an E6/E6-AP. In a preferred embodiment, the *UBC* inhibitor is a mechanism based inhibitor which chemically alters the enzyme, e.g. covalently binds Cys-85 of hUbCE or Cys-93 of rapUBC, and which is a specific inhibitor of that enzyme, e.g. has an inhibition constant 10-fold, 100-fold, or more preferably, 1000-fold different for human E2 enzymes other than the subject *UBC* enzyme. Inhibitor specificity can be improved, for example, by utilizing specificity subsites of the hUbCE enzyme involved in interactions between hUbCE and an E6/E6AP complex, or hUbCE and an E1 enzyme, which are unique to one of those complexes relative to other human E2 enzymes. Similar approaches can also be used to screen for drugs agonistic or antagonistic to rapUBC activities.

Assays for the measurement of ubiquitination can be generated in many different forms, and include assays based on cell-free systems, e.g. purified proteins or cell lysates, as well as cell-based assays which utilize intact cells. Assays as described herein can be used in conjunction with the subject E2 enzymes to generate a ubiquitin-conjugating system for

detecting agents able to inhibit particular E2-mediated ubiquitination of a cellular or viral regulatory proteins. Such inhibitors can be used, for example, in the treatment of proliferative and/or differentiative disorders, to modulate apoptosis, and in the treatment of viral infections, such by adenoviruses or papillomaviruses. Similar assay systems can be constructed for the fungal homologs in order to detect inhibitors which may serve as anti-fungal agents. In preferred embodiments, the assay system employed for identifying anti-fungal agents are run side-by-side with the analogous assay system derived with the mammalian homolog of the UBC, e.g. hUbCE or rapUBC. Differential screening assays can be used to exploit any difference in mechanism or specificity between mammalian *UBCs* and yeast *UBCs* (including other yeast E2 enzymes) in order to identify agents which display a statistically significant increase in specificity for inhibiting the yeast enzymes relative to the mammalian enzymes. Thus, lead compounds which act specifically on pathogens, such as fungus involved in mycotic infections, can be developed.

In many drug screening programs which test libraries of compounds and natural extracts, high throughput assays are desirable in order to maximize the number of compounds surveyed in a given period of time. Assays which are performed in cell-free systems, such as may be derived with purified or semi-purified proteins or with lysates, are often preferred as "primary" screens in that they can be generated to permit rapid development and relatively easy detection of an alteration in a molecular target which is mediated by a test compound. Moreover, the effects of cellular toxicity and/or bioavailability of the test compound can be generally ignored in the *in vitro* system, the assay instead being focused primarily on the effect of the drug on the molecular target as may be manifest in an alteration of binding affinity with other proteins or change in enzymatic properties of the molecular target. Accordingly, potential E2 inhibitors can be detected in a cell-free assay generated by consitution of a functional ubiquitin-protein ligase system in a cell lysate, such as generated by charging a ubiquitin-depleted reticulocyte lysate (Hersko et al. (1983) *J Biol Chem* 258:8206-6214) with one of the subject UBC enzymes and, as needed, an E1 enzyme, an E3 enzyme (cellular or viral in origin), ubiquitin, and a substrate for *UBC*-dependent ubiquitination. In an alternative format, the assay can be derived as a reconstituted protein mixture which, as described below, offers a number of benefits over lysate-based assays.

In yet other embodiments, the present assay comprises an *in vivo* ubiquitin-conjugating system, such as a cell able to conduct the regulatory protein through at least a portion of a ubiquitin-mediated proteolytic pathway.

The level of ubiquitination of the substrate protein brought about by the system is measured in the presence and absence of a candidate agent, and a decrease in the level ubiquitin conjugation is indicative of an inhibitory activity for the candidate agent. As described below, the level of ubiquitination of the regulatory protein can be measured by determining the actual concentration of protein:ubiquitin conjugates formed; or inferred by

detecting some other quality of the subject protein affected by ubiquitination, including the proteolytic degradation of the protein. A statistically significant decrease in ubiquitination of the target protein in the presence of the test compound is indicative of the test compund being an inhibitor of E2-dependent ubiquitin conjugation.

In preferred *in vitro* embodiments of the present assay, the ubiquitin-conjugating system comprises a reconstituted protein mixture of at least semi-purified proteins. By semi-purified, it is meant that the proteins utilized in the reconstituted mixture have been previously separated from other cellular or viral proteins. For instance, in contrast to cell lysates, the proteins involved in conjugation of ubiquitin to a target protein, together with the target protein, are present in the mixture to at least 50% purity relative to all other proteins in the mixture, and more preferably are present at 90-95% purity. In certain embodiments of the subject method, the reconstituted protein mixture is derived by mixing highly purified proteins such that the reconstituted mixture substantially lacks other proteins (such as of cellular or viral origin) which might interfere with or otherwise alter the ability to measure specific ubiquitination or ubiquitin-mediated degradation of the target regulatory protein.

Each of the protein components utilized to generate the reconstituted ubiquitin-conjugating system are preferably isolated from, or otherwise substantially free of, other proteins normally associated with the proteins in a cell or cell lysate. The term "substantially free of other cellular proteins" (also refered to herein as "contaminating proteins") is defined as encompassing individual preparations of each of the component proteins comprising less than 20% (by dry weight) contaminating protein, and preferably comprises less than 5% contaminating protein. Functional forms of each of the component proteins can be prepared as purified preparations by using a cloned gene as described in the attached examples. By "purified", it is meant, when referring to the component proteins preparations used to generate the reconstituted protein mixture, that the indicated molecule is present in the substantial absence of other biological macromolecules, such as other proteins (particularly other proteins which may substantially mask, diminish, confuse or alter the characteristics of the component proteins either as purified preparations or in thier function in the subject reconstituted mixture). The term "purified" as used herein preferably means at least 80% by dry weight, more preferably in the range of 95-99% by weight, and most preferably at least 99.8% by weight, of biological macromolecules of the same type present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 5000, can be present). The term "pure" as used herein preferably has the same numerical limits as "purified" immediately above. "Isolated" and "purified" do not encompass either protein in its native state (e.g. as a part of a cell), or as part of a cell lysate, or that have been separated into components (e.g., in an acrylamide gel) but not obtained either as pure (e.g. lacking contaminating proteins) substances or solutions. The term isolated as used herein also refers to a component protein that is substantially free of cellular material or culture medium when

produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized.

With respect to measuring ubiquitination, the purified protein mixture can substantially lack any proteolytic activity which would degrade the target protein and/or components of the ubiquitin conjugating system. For instance, the reconstituted system can be generated to have less than 10% of the proteolytic activity associated with a typical reticulocyte lysate, and preferably no more than 5%, and most preferably less than 2%. Alternatively, the mixture can be generated to include, either from the onset of ubiquitination or from some point after ubiquitin conjugation of the regulatory protein, a ubiquitin-dependent proteolytic activity, such as a purified proteosome complex, that is present in the mixture at measured amounts.

In the subject method, ubiquitin conjugating systems derived from purified proteins hold a number of significant advantages over cell lysate or wheat germ extract based assays (collectively referred to hereinafter as "lysates"). Unlike the reconstituted protein system, the synthesis and destruction of the target protein cannot be readily controlled for in lysate-based assays. Without knowledge of particular kinetic parameters for Ub-independant and Ub-dependent degradation of the target protein in the lysate, discerning between the two pathways can be extremely difficult. Measuring these parameters, if at all possible, is further made tedious by the fact that cell lysates tend to be inconsistent from batch to batch, with potentially significant variation between preparations. Evaluation of a potential inhibitor using a lysate system is also complicated in those circumstances where the lysate is charged with mRNA encoding the target protein, as such lysates may continue to synthesize the protein during the assay, and will do so at unpredictable rates.

Using similar considerations, knowledge of the concentration of each component of the ubiquitin conjugation pathway can be required for each lysate batch, along with the degradative kinetic data, in order to determine the necessary time course and calculate the sensitivity of experiments performed from one lysate preparation to the next.

Furthermore, the lysate system can be unsatisfactory where the target protein itself has a relatively short half-life, especially if due to degradative processes other than the ubiquitin-mediated pathway to which an inhibitor is sought. For example, in assays for an inhibitor of HPV-induced ubiquitination of p53, lysate based systems can be difficult to use, in addition to the reasons set forth above, due to the short half-life of p53 even in extracts which lack HPV proteins. In such systems, the ability to measure HPV-mediated ubiquitination of p53 is made difficult by the already rapid, ongoing degradation of p53 presumably occurring by proteolytic processes which are not mediated by any HPV proteins.

The use of reconstituted protein mixtures allows more careful control of the reaction conditions in the ubiquitin-conjugating system. Moreover, the system can be derived to favor discovery of inhibitors of particular steps of the ubiquitination process. For instance, a reconstituted protein assay can be generated which does not facilitate degradation of the

ubiquitinated protein. The level of ubiquitin conjugated protein can easily be measured directly in such as system, both in the presence and absence of a candidate agent, thereby enhancing the ability to detect a ubiquitination inhibitor. Alternatively, the Ub-conjugating system can be allowed to develop a steady state level of regulatory protein:Ub conjugates in the absence of a proteolytic activity, but then shifted to a degradative system by addition of purified Ub-dependent proteases. Such degradative systems would be amenable to identifying proteosome inhibitors.

The purified protein mixture includes a purified preparation of the regulatory protein and ubiquitin under conditions which drive the conjugation of the two molecules. For instance, the mixture can include a ubiquitin-activating enzyme (E1), a ubiquitin-conjugating enzyme (E2), and a nucleotide triphosphate (e.g. ATP). Alternatively, the E1 enzyme, the ubiquitin, and the nucleotide triphosphate can be substituted in the system with a pre-activated ubiquitin in the form of an E1::Ub conjugate. Likewise, a pre-activated ubiquitin can instead comprise an E2::Ub conjugate which can directly transfer the pre-activated ubiquitin to the target protein substrate.

Furthermore, the reconstituted mixture can also be generated to include at least one auxiliary substrate recognition protein (E3) which may be, for example, of cellular or viral origin. In illustrative embodiments described below, in order to generate an assay which approximates the ubiquitination of p53 in HPV-16 or HPV-18 infected cells, the reconstitutated ubiquitin conjugating system may further include an E6 protein of HPV origin, as well as an E6-associated protein (E6-AP) of cellular origin.

Ubiquitination of the target regulatory protein via an *in vitro* ubiquitin-conjugating system, in the presence and absence of a candidate inhibitor, can be accomplished in any vessel suitable for containing the reactants. Examples include microtitre plates, test tubes, and micro-centrifuge tubes. In certain embodiments of the present assay, the *in vitro* assay system is generated to lack the ability to degrade the ubiquitinated target protein. In such an embodiments, a wide range of detection means can be practiced to score for the presence of the ubiquitinated protein.

In one embodiment of the present assay, the products of a non-degradative ubiquitin-conjugating system are separated by gel electrophoresis, and the level of ubiquitinated target protein assessed, using standard electrophaesis protocols, by measuring an increase in molecular weight of the target protein that corresponds to the addition of one or more ubiquitin chains. For example, one or both of the target protein and ubiquitin can be labeled with a radioisotope such as ^{35}S, ^{14}C, or ^{3}H, and the isotopically labeled protein bands quantified by autoradiographic techniques. Standardization of the assay samples can be accomplished, for instance, by adding known quantities of labeled proteins which are not themselves subject to ubiquitination or degradation under the conditions which the assay is performed. Similarly, other means of detecting electrophoretically separated proteins can be

employed to quantify the level of ubiquitination of the regulatory protein, including immunoblot analysis using antibodies specific for either the regulatory protein or ubiquitin, or derivatives thereof. As described below, the antibody can be replaced with another molecule able to bind one of either the regulatory protein or ubiquitin. By way of illustration, one embodiment of the present assay comprises the use of biotinylated ubiquitin in the conjugating system. The biotin label is detected in a gel during a subsequent detection step by contacting the electrophoretic products (or a blot thereof) with a streptavidin-conjugated label, such as a streptavidin linked fluorochrome or enzyme, which can be readily detected by conventional techniques. Moreover, where a reconstituted protein mixture is used (rather than a lysate) as the conjugating system, it may be possible to simply detect the regulatory protein and ubiquitin conjugates in the gel by standard staining protocols, including coomassie blue and silver staining.

In another embodiment, an immunoassay or similar binding assay, is used to detect and quantify the level of ubiquitinated regulatory protein produced in the ubiquitin-conjugating system. Many different immunoassay techniques are amenable for such use and can be employed to detect and quantitate the regulatory protein:Ub conjugates. For example, the wells of a microtitre plate (or other suitable solid phase) can be coated with an antibody which specifically binds one of either the regulatory protein or ubiquitin. After incubation of the ubiquitin-conjugated system with and without the candidate agent, the products are contacted with the matrix bound antibody, unbound material removed by washing, and ubiquitin conjugates of the regulatory protein specifically detected. To illustrate, if an antibody which binds the regulatory protein is used to sequester the protein on the matrix, then a detectable anti-ubiquitin antibody can be used to score for the presence of ubiquitinated regulatory protein on the matrix.

However, it will be clear to those skilled in the art that the use of antibodies in these binding assays is merely illustrative of binding molecules in general, and that the antibodies are readily substituted in the assay with any suitable molecule that can specifically detect one of either the substrate protein or the ubiquitin. As described below, a biotin-derivative of ubiquitin can be used, and streptavidin (or avidin) employed to bind the biotinylated ubiquitin. In an illustrative embodiment, wells of a microtitre plate are coated with streptavidin and contacted with the developed ubiquitin-conjugating system under conditions wherein the biotinylated ubiquitin binds to and is sequestered in the wells. Unbound material is washed from the wells, and the level of regulatory protein (bound to the matrix via a conjugated ubiquitin moiety) is detected in each well. Alternatively, the microtitre plate wells can be coated with an antibody (or other binding molecule) which binds and sequesters the regulatory protein on the solid support, and detection of ubiquitinated conjugates of the matrix-bound regulatory protein are subsequently carried out using a detectable streptavidin derivative, such as an alkaline phosphatase/streptavidin complex.

In similar fashion, epitope-tagged ubiquitin, such as myc-ub (see Ellison et al. (1991) *J. Biol. Chem.* 266:21150-21157; ubiquitin which includes a 10-residue sequence encoding a protein of c-myc) can be used in conjunction with antibodies to the epitope tag. A major advantage of using such an epitope-tagged ubiquitin approach for detecting Ub:protein conjugates is the ability of an N-terminal tag sequences to inhibit ubiquitin-mediated proteolysis of the conjugated regulatory protein.

Other ubiquitin derivatives include detectable labels which do not interfere greatly with the conjugation of ubiquitin to the regulatory protein. Such detectable lables can include fluorescently-labeled (e.g. FITC) or enzymatically-labeled ubiquitin fusion proteins. These derivatives can be produced by chemical cross-linking, or, where the label is a protein, by generation of a fusion protein. Several labeled ubiquitin derivatives are commercially available.

Likewise, other binding molecules can be employed in place of the antibodies that bind the regulatory protein. For example, the regulatory protein can be generated as a glutathione-S-transferase (GST) fusion protein. As a practical matter, such GST fusion protein can enable easy purification of the regulatory protein in the preparation of components of the ubiquitin-conjugating system (see, for example, *Current Protocols in Molecular Biology,* eds. Ausubel et al. (NY: John Wiley & Sons, 1991); Smith et al. (1988) *Gene* 67:31; and Kaelin et al. (1992) *Cell* 70:351) Moreover, glutathione derivatized matrices (e.g. glutathione-sepharose or glutathione-coated microtitre plates) can be used to sequester free and ubiquitinated forms of the regulatory protein from the ubiguitin-conjugating system, and the level of ubiquitin immobilized can be measured as described. Likewise, where the matrix is generated to bind ubiquitin, the level of sequestered GST-regulatory protein can be detected using agents which bind to the GST moiety (such as anti-GST antibodies), or, alternatively, using agents which are enzymatically acted upon by GST to produce detectable products (e.g. 1-chloro-2,4-dinitrobenzene; Habig et al. (1974) *J Biol Chem* 249:7130). Similarly, other fusion proteins involving the regulatory protein and an enzymatic activity are contemplated by the present method. For example, fusion proteins containing β-galactosidase or luciferase, to name but a few, can be employed as labels to determine the amount of regulatory protein sequestered on a matrix by virtue of a conjugated ubiquitin chain.

Moreover, such enzymatic fusion proteins can be used to detect and quantitate ubiquitinated regulatory protein in a heterogeneous assay, that is one which does not require separation of the components of the conjugating system. For example, ubiquitin conjugating systems can be generated to have a ubiquitin-dependent protease which degrades the regulatory protein. The enzymatic activity of the fusion protein provides a detectable signal, in the presence of substrate, for measuring the level of the regulatory protein ubiquitination. Similarly, in a non-degradative conjugating system, ubiquitination of the regulatory protein

portion of the fusion protein can allosterically influence the enzymatic activity associated with the fusion the protein and thereby provides a means for monitoring the level of ubiquitin conjugation.

In binding assay-type detection steps set out above, the choice of which of either the regulatory protein or ubiquitin should be specifically sequestered on the matrix will depend on a number of factors, including the relative abundance of both components in the conjugating system. For instance, where the reaction conditions of the ubiquitin conjugating system provide ubiquitin at a concentration far in excess of the level of the regulatory protein, (e.g., one order of magnitude or greater) sequestering the ubiquitin and detecting the amount of regulatory protein bound with the ubiquitin can provide less dynamic range to the detection step of the present method than the converse embodiment of sequestering the regulatory protein and detecting ubiquitin conjugates from the total regulatory protein bound to the matrix. That is, where ubiquitin is provided in great excess relative to the regulatory protein, the percentage of ubiquitin conjugated regulatory protein in the total ubiquitin bound to the matrix can be small enough that any diminishment in ubiquitination caused by an inhibitor can be made difficult to detect by the fact that, for example, the statistical error of the system (e.g. the noise) can be a significant portion of the measured change in concentration of bound regulatory protein. Furthermore, it is clear that manipulating the reaction conditions and reactant concentrations in the ubiquitin-conjugating system can be carried out to provide, at the detection step, greater sensitivity by ensuring that a strong ubiquitinated protein signal exists in the absence of any inhibitor.

Furthermore, drug screening assays can be generated which do not measure ubiquitination *per se*, but rather detect inhibitory agents on the basis of their ability to interfere with binding of one of the subject UBC proteins with any other immediate upstream or downstream component of the ubiquitin conjugation pathway. In an exemplary binding assay, the compound of interest is contacted with a mixture generated from an isolated and purified E2 protein, such as *hUbCE* or *rapUBC*, and another component of the ubiquitin conjugation pathway which binds to one of the UBC proteins (e.g. a "*UBC*-associated protein"), such as an E1 or E3 protein, or other cellular substrates of the subject *UBC*. Detection and quantification of E2 complexes provides a means for determining the compound's efficacy at inhibiting (or potentiating) complex formation between the *UBC*-associated protein and the *UBC* protein. The efficacy of the compound can be assessed by generating dose response curves from data obtained using various concentrations of the test compound. Moreover, a control assay can also be performed to provide a baseline for comparison. In the control assay, isolated and purified *UBC* is added to a composition containing the *UBC*-associated protein, and the formation of *UBC*-containing complexes is quantitated in the absence of the test compound.

Complex formation between the *UBC* protein and *UBC*-associated protein may be detected by a variety of techniques, many of which are effectively described above. For instance, modulation in the formation of complexes can be quantitated using, for example, detectably labelled proteins (e.g. radiolabelled, fluorescently labelled, or enzymatically labelled), by immunoassay, or by chromatographic detection.

Typically, it will be desirable to immobilize either *UBC* or the *UBC*-associated protein to facilitate separation of complexes from uncomplexed forms of one of the proteins, as well as to accommodate automation of the assay. In an illustrative embodiment, a fusion protein can be provided which adds a domain that permits the protein to be bound to an insoluble matrix. For example, GST/*UBC* fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtitre plates, which are then combined with the *UBC*-associated protein, e.g. an ^{35}S-labeled *UBC*-associated protein, and the test compound and incubated under conditions conducive to complex formation. Following incubation, the beads are washed to remove any unbound *UBC*-associated protein, and the matrix bead-bound radiolabel determined directly (e.g. beads placed in scintilant), or in the supernantant after the *UBC* complexes are dissociated, e.g. when microtitre plaste is used. Alternatively, after washing away unbound protein, the complexes can be dissociated from the matrix, separated by SDS-PAGE gel, and the level of *UBC*-associated protein found in the matrix-bound fraction quantitated from the gel using standard electrophoretic techniques.

In still further embodiments of the present assay, the ubiquitin-conjugating system is generated in whole cells, taking advantage of cell culture techniques to support the subject assay. For example, as described below, the ubiquitin-conjugating system (including the target protein and detection means) can be constituted in a eukaryotic cell culture system, including mammalian and yeast cells. Advantages to generating the subject assay in an intact cell include the ability to detect inhibitors which are functional in an environment more closely approximating that which therapeutic use of the inhibitor would require, including the ability of the agent to gain entry into the cell. Furthermore, certain of the *in vivo* embodiments of the assay, such as examples given below, are amenable to high through-put analysis of candidate agents.

The components of the ubiquitin-conjugating system, including the regulatory protein, can be endogenous to the cell selected to support the assay. Alternatively, some or all of the components can be derived from exogenous sources. For instance, a virally derived E3 protein, such as an HPV E6 protein, can be introduced into the cell by recombinant techniques (such as through the use of an expression vector), as well as by microinjecting the E3 protein itself or mRNA encoding the E3 protein.

In any case, the cell is ultimately manipulated after incubation with a candidate inhibitor in order to facilitate detection of ubiquitination or ubiquitin-mediated degradation of

the regulatory protein. As described above for assays performed in reconstituted protein mixtures or lysate, the effectiveness of a candidate inhibitor can be assessed by measuring direct characteristics of the regulatory protein, such as shifts in molecular weight by electrophoretic means or detection in a binding assay. For these embodiments, the cell will typically be lysed at the end of incubation with the candidate agent, and the lysate manipulated in a detection step in much the same manner as might be the reconstituted protein mixture or lysate.

Indirect measurement of ubiquitination of the target protein can also be accomplished by detecting a biological activity associated with the regulatory protein that is either attenuated by ubiquitin-conjugation or destroyed along with the regulatory protein by ubiquitin-dependent proteolytic processes. As set out above, the use of fusion proteins comprising the regulatory protein and an enzymatic activity are representative embodiments of the subject assay in which the detection means relies on indirect measurement of ubiquitination of the regulatory protein by quantitating an associated enzymatic activity.

Where the regulatory protein has a relatively short half-life due to ubiquitin-dependent or independent degradation in the cell, preferred embodiments of the assay either do not require cell lysis, or, alternatively, generate a longer lived detection signal that is independent of the regulatory protein's fate after lysis of the cell. With respect to the latter embodiment, the detection means can comprise, for example, a reporter gene construct which includes a positive transcriptional regulatory element that binds and is responsive to the regulatory protein. For instance, where the regulatory protein of interest is p53, p53 responsive elements can be used to construct the reporter gene. These include p53 binding sequences set out in Example 7 and Figure 9, as well as a creatine kinase enhancer, an interleukin-6 promoter, a c-fos promoter, a β-actin promoter, an hsc70 promoter, a c-jun promoter, a p53 promoter, and a CYC1 hybrid promoter containing a p53-binding sequence. The gene product is a detectable label, such as luciferase or β-galactosidase, and is produced in the intact cell. The label can be measured in a subsequent lysate of the cell. However, the lysis step is preferably avoided, and providing a step of lysing the cell to measure the label will typically only be employed where detection of the label cannot be accomplished in whole cells.

Moreover, in the whole cell embodiments of the subject assay, the reporter gene construct can provide, upon expression, a selectable marker. For instance, the product of the reporter gene can be an enzyme which confers resistance to antibiotic or other drug, or an enzyme which complements a deficiency in the host cell (i.e. thymidine kinase or dihydrofolate reductase). To illustrate, the aminoglcycoside phosphotransferase encoded by the bacterial transposon gene Tn5 *neo* can be placed under transcriptional control of a promoter element responsive to the level of target regulatory protein present in the cell. Thus, the level of expression of the phenotypic marker gene is lower in the absence of an

inhibitor of ubiquitin-mediated proteolysis of the regulatory protein, and such inhibitors can be detected in the assay by an ability to confer the measured phenotypic trait. Such embodiments of the subject assay are particularly amenable to high through-put analysis in that proliferation of the cell can provide a simple measure of inhibition of the ubiquitin-mediated degradation of the regulatory protein.

In yet a further embodiment of the subject assay, the ubiquitin-conjugating system comprises a cell in which the biological activity of the target regulatory protein has been substantially impaired, the impairment being the result of abnormal ubiquitination of the regulatory protein. The cell, in the presence or absence of a candidate inhibitor, is subject to growth conditions that would ordinarily required the function of the regulatory protein for viability of the cell. Thus, an inhibitor of the ubiquitin-mediated degradation of the regulatory protein would restore the biological activity of the protein to the cell, and could easily be detected by the ability of the cell to proliferate. To further illustrate, the impairment of the regulatory protein can be the result of over expression of a cellular protein of the ubiquitin pathway, such as an E2 or E3 protein, which results in hyper-ubiquitination of the regulatory protein. Alternatively, the impairment can result from non-cellular agents, such as viral proteins, which increase the ubiquitin-mediated degradation of the regulatory protein. For example, as described above, expression of the HPV E6 protein can result in decreased levels of p53 in the cell due to the increased ubiquitin-dependent inactivation of the protein.

In embodiments of the subject method in which the target regulatory protein ordinarily acts as a negative regulator of mitotic events, impairment of the regulatory protein can result in a hyper-mitotic cell. The term hyper-mitotic cell denotes a cell having an impaired cell-cycle checkpoint which can allow the cell to proceed abherently toward subsequent mitotic stages and ultimately inhibits faithful proliferation of the cell. In the present of an agent able to inhibit the ubiquitin-mediated inactivation of the regulatory protein, progression of the hyper-mitotic cell through the cell-cycle can be reestablished under control of the regulatory protein and permit the cell to appropriately proliferate.

To illustrate, a p53-impaired cell can be generated by expression of the HPV viral protein E6. The concomitant decrease in p53 levels brought about by E6 expression does not in and of itself cause abherent mitotic events to occur. However, exposure of the impaired cell to an agent (i.e. chemical or environmental) that ordinarily induces cell-cycle arrest at the p53 checkpoint can result in inappropriate exit of the cell from the chemically or environmentally induced arrest. This type of checkpoint override can ultimately be lethal to the cell. Such arresting agents can include exposure to DNA damaging radiation or DNA damaging agents; inhibition of DNA synthesis or repairmen using DNA polymerase inhibitors such as hydroxyurea or aphidicolin; topoisomerase inhibitors such as 4'-dimethylepipodophyllotoxin (VM-26); or agents which interfere with microtubule assembly, such as nocadazole and taxol.

With respect to embodiments in which the regulatory protein ordinarily acts as a mitotic activator, impairment of the protein's activity by ubiquitination can generate a hypo-mitotic cell in which progression of the cell through at least a portion of the cell-cycle is repressed. In the presence of an inhibitor of ubiquitin-dependent degradation of the regulatory protein, the activity of the mitotic activator is restored and the cell can proliferate at an greater rate relative to the untreated cell. Agents to be tested for their ability to act as inhibitor of ubiquitin-dependent degradation of the regulatory protein in the present assay can be those produced by bacteria, yeast or other organisms, or those produced chemically.

With respect to sources for the proteins constituting the ubiquitin-conjugating system, particularly to generate the reconstituted protein mixture, many species of the enzymes and other proteins involved in ubiquitination have been identified, and in a significant number of instances, have been cloned so that recombinant sources exist. Isolation of enzymes of the ubiquitin-conjugating system has been greatly assisted by "covalent" ubiquitin-affinity chromatography (Crechanover et al. (1982) *J. Biol. Chem.* 257:2537-2542; and Pickart et al. (1985) *J. Biol. Chem.* 260:1573-1581). This method takes advantage of the fact that the E1 enzyme is capable of forming a thiol ester with immobilized ubiquitin (e.g. ubiquitin-sepharase) in the presence of ATP. As described in Example 2, such a protocol can be used to purify recombinantly expressed E1. Moreover, E1 enzymes bound to the immobilized ubiquitin can be exchanged with E2 enzymes. Thus, both E1 and E2 enzymes can be specifically purified on such columns, and can be recovered after elution with, for example, dithiothreitol. Under appropriate elution conditions, ubiquitin activated E1 or E2 complexes can be isolated and, as described herein, used in the present assay to increase the selectivity of the assay for an inhibitor of a particular step of ubiquitin-conjugation. Moreover, with minor changes, this protocol can be used to isolate E1:Ub or E2:Ub conjugates (e.g. activated ubiquitin conjugates) for use in the reconstituted protein mixture.

Identification of enzymes involved in the ubiquitin pathway from different sources have facilitated the cloning of corresponding genes. For instance, genes encoding E1 enzymes have been cloned from various organisms (see, for example, Adams et al. (1992) *Nature* 355:632-634; Handley et al. (1991) *PNAS* 88:258-262; Handley et al. (1991) *PNAS* 88:7456; Hatfield et al. (1990) *J. Biol. Chem.* 265:15813-15817; Kay et al. (1991) *Nature* 354:486-489; McCrath eg al. (1991) *EMBO J* 10:227-236; Mitchell et al. (1991) *Nature* 354:483-486; and Zacksenhaus et al. (1990) *EMBO J* 9:2923-2929). The sequences of various cloned E1 enzymes predict proteins of roughly 100kd, and which contain the nucleotide-binding consensus sequence Gly-Xaa-Gly-Xaa-Xaa-Gly (McGrath et al. (1991) *EMBO J* 10:227-236). For example, the gene *UBA1* has been cloned from *S. cerevisiae* and shown to encode a 114 kd E1 enzyme (McGrath et al., *supra*). Moreover, more than one E1 species has been detected in the same cell-type, suggesting that two or more different E1 enzymes can exist. It is not yet known whether the different E1 enzymes are enzymatically

similar, or if they collaborate with specific sets of ubiquitin-conjugating enzymes. In either case, each of the E1 species can be used to generate the ubiquitin-conjugating system of the subject method.

In contrast to the ubiquitin-activating enzyme (E1), where it is generally believed that there are relatively few different species of the enzyme in a given cell, eukaryotic cells can express a large and diverse array of E2 enzymes. This remarkable variety of E2 enzymes, along with experimental evidence, has implicated the E2 enzyme as the principle determinant of substrate selectivity in the ubiquitin system. The E2 enzyme, as set out above, catalyzes isopeptide bond formation between ubiquitin and substrate proteins, either with or without the aid of a substrate recognition factor (ubiquitin-ligase protein; E3). Accordingly, in addition to the subject UBC proteins, e.g., UbCE and rapUBC, the subject assays can be performed with other E2 enzymes. For instance, several major species of E2 enzymes have been identified and purifed by ubiquitin-affinity chromatography of extracts from rabbit reticulocytes (Pickart et al. (1985) *J Biol Chem* 260:1573-1581), yeast (Jentsch et al. (1987) *Nature* 329:131-134), and wheat (Sullivan et al. (1989) *PNAS* 86:9861-9865). Furthermore, many genes encoding E2 enzymes have been cloned and characterized, most notably in the yeast *Sacchromyces cerevisiae*, where the phenotypic consequences of their inactivation can be readily assessed. More than 10 yeast E2 genes have been identified to date (see Jentsch (1992) *Annu Rev Genet* 26:179-207; and Jentsch (1992) *Trends Cell Biol* 2:98-103), and there evidence for over 20 E2 genes in the plant *Arabipodopsis* (Cook et al. (1992) *J Biol Chem* 267:15116-15121). Additionally, E2 enzymes have been cloned from nematode (Zhen et al. (1993) *Mol Cell Biol* 13:1371-1377), drosophila (Muralidher et al. (1993) *Neuron* 11:253-266; and Koken et al. (1991) *PNAS* 88:3832-3836), bovine (Chen et al. (1991) *J Biol Chem* 266:15698-15704) and human cells (Koken et al. (1992) *Genomics* 12:447-453; Koken et al. (1991) *PNAS* 88:8865-8869; and Schneider et al. (1990) *EMBO J* 9:1431-1435). Other E2 enzymes can be substituted in the subject assays in place of the UbCE or rapUBC proteins of the present invention, or can be provided in addition to a UbCE or rapUBC protein, e.g., in a differential screening assay.

Some ubiquitin-conjugating enzymes require accessory factors, E3 proteins, for the recognition of certain protein substrates. Two E3 proteins, E3α and E3β, have been identified from rabbit reticulocytes (Reiss et al. (1989) *J. Biol. Chem.* 264:10378-10383; and Reiss et al. (1990) *J. Biol. Chem.* 265:3685-3690). A yeast gene (UBR1) encoding an E3 functionally similar to rabbit E3α has also been cloned (Bartel et al. (1990) *EMBO J* 9:3179-3189). Rabbit E3α and yeast UBR1 bind to substrates with N-terminal amino acid residues that are basic or have bulky hydrophobic side chains, while the E3β recognizes small unchanged residues at the N-terminus of substrates. In addition to the E3 proteins that recognize the N-terminus of protein substrates, other E3 proteins (collectively know as E3γ, capable of recognizing internally located signals, have been suspected.

Proteins that facilitate ubiquitin-conjugation reactions without physically interacting with E2 enzymes can also be classed as E3 proteins. By this definition, the E6 oncoprotein of the papillomavirus is regarded as an E3 protein, as binding of E6 triggers the ubiquitination and degradation of p53. For example, recombinant E6 protein from the high-risk HPV-18 (SEQ ID No.14), as well as the cellular factor E6-AP (SEQ ID No.15), are available for use in the subject assay.

The regulatory protein provided in the subject assay can be derived by purification from a cell in which it is exogenously expressed, or from a recombinant source of the protein. For example, cDNA clones are available for a number of regulatory proteins, including p53 (Oren et al. (1983) *EMBO J* 2:1633-1639); p27 (Polyak et al. (1994) *Cell* 78:59-66; and Toyoshima et al. (1994) *Cell* 78:67-74); c-myc (Hann et al. (1988) *Cell* 52:185-195); N-myc (Curran et al. (1987) *Oncogene* 2:79-84); MATα2 (Hochstrasser et al. (1990) *Cell* 61:697-708); and E1A (Salvicek et al. (1988) *EMBO J* 7:3171-3180).

Additionally, the subject ubiquitin conjugating enzyme can be used to generate an interaction trap assay for subsequently detecting inhibitors of hUbCE or rapUBC biological activity (see, for example, U.S. Patent No: 5,283,317; PCT publication WO94/10300; Zervos et al. (1993) *Cell* 72:223-232; Madura et al. (1993) *J Biol Chem* 268:12046-12054; Bartel et al. (1993) *Biotechniques* 14:920-924; and Iwabuchi et al. (1993) *Oncogene* 8:1693-1696) In an illustrative embodiment, *Saccharomyces cerevisiae* YPB2 cells are transformed simultaneously with a plasmid encoding a GAL4db-hUbCE fusion and with a plasmid encoding the GAL4ad domain fused to p53 or E6AP. Moreover, the strain is transformed such that the GAL4-responsive promoter drives expression of a phenotypic marker. For example, the ability to grow in the absence of histidine can depends on the expression of the HIS3 gene if it is under control of a GAL4-responsive promoter and, therefore, indicates that a functional GAL4 activator has been reconstituted through the interaction of hUbCE and p53 or E6AP. Thus, agent able to inhibit hUbCE interaction with one of these proteins will result in yeast cells unable to growth in the absence of histidine. Alternatively, the phenotypic marker can be one which provides a negative selection when expressed such that agents which disrupt the hUbCE interactions confer positive growth selection to the cells.

Another aspect of the present invention concerns three-dimensional molecular models of the subject UBC proteins, and their use as templates for the design of agents able to inhibit at least one biological activity of the ubiquitin conjugating enzyme. An integral step to our approach to designing inhibitors of the subject ubiquitin-conjugating enzyme involves construction of computer graphics models of the ubiquitin conjugating enzyme which can be used to design pharmacophores by rational drug design. For instance, for an inhibitor to interact optimally with the subject enzyme, it will generally be desirable that it have a shape which is at least partly complimentary to that of a particular binding site of the enzyme, as for example those portions of the human ubiquitin conjugating enzyme which are involved in

recognition of ubiquitin, an E1 enzyme, an E3 protein(s) such as E6 or E6AP, or a downstream target of the pathway, such as p53. Additionally, other factors, including electrostatic interactions, hydrogen bonding, hydrophobic interactions, desolvation effects, and cooperative motions of ligand and enzyme, all influence the binding effect and should be taken into account in attempts to design bioactive inhibitors.

As described in Example 9, a computer-generated molecular model of the subject enzymes can be created. In preferred embodiments, at least the Cα-carbon positions of the *UBC* sequence of interest are mapped to a particular coordinate pattern, such as the coordinates for hUbCE shown in Figure 1, by homology modeling, and the structure of the protein and velocities of each atom are calculated at a simulation temperature (T_o) at which the docking simulation is to be determined. Typically, such a protocol involves primarily the prediction of side-chain conformations in the modeled protein, while assuming a main-chain trace taken from a tertiary structure such as provided in Figure 1. Computer programs for performing energy minimization routines are commonly used to generate molecular models. For example, both the CHARMM (Brooks et al. (1983) *J Comput Chem* 4:187-217) and AMBER (Weiner et al (1981) *J. Comput. Chem.* 106: 765) algorithms handle all of the molecular system setup, force field calculation, and analysis (see also, Eisenfield et al. (1991) *Am J Physiol* 261:C376-386; Lybrand (1991) *J Pharm Belg* 46:49-54; Froimowitz (1990) *Biotechniques* 8:640-644; Burbam et al. (1990) *Proteins* 7:99-111; Pedersen (1985) *Environ Health Perspect* 61:185-190; and Kini et al. (1991) *J Biomol Struct Dyn* 9:475-488). At the heart of these programs is a set of subroutines that, given the position of every atom in the model, calculate the total potential energy of the system and the force on each atom. These programs may utilize a starting set of atomic coordinates, such as the model coordinates provided in Figure 1, the parameters for the various terms of the potential energy function, and a description of the molecular topology (the covalent structure). Common features of such molecular modeling methods include: provisions for handling hydrogen bonds and other constraint forces; the use of periodic boundary conditions; and provisions for occasionally adjusting positions, velocities, or other parameters in order to maintain or change temperature, pressure, volume, forces of constraint, or other externally controlled conditions.

Most conventional energy minimization methods use the input data described above and the fact that the potential energy function is an explicit, differentiable function of Cartesian coordinates, to calculate the potential energy and its gradient (which gives the force on each atom) for any set of atomic positions. This information can be used to generate a new set of coordinates in an effort to reduce the total potential energy and, by repeating this process over and over, to optimize the molecular structure under a given set of external conditions. These energy minimization methods are routinely applied to molecules similar to the subject UBC proteins as well as nucleic acids, polymers and zeolites.

In general, energy minimization methods can be carried out for a given temperature, T_i, which may be different than the docking simulation temperature, T_o. Upon energy minimization of the molecule at T_i, coordinates and velocities of all the atoms in the system are computed. Additionally, the normal modes of the system are calculated. It will be appreciated by those skilled in the art that each normal mode is a collective, periodic motion, with all parts of the system moving in phase with each other, and that the motion of the molecule is the superposition of all normal modes. For a given temperature, the mean square amplitude of motion in a particular mode is inversely proportional to the effective force constant for that mode, so that the motion of the molecule will often be dominated by the low frequency vibrations.

After the molecular model has been energy minimized at T_i, the system is "heated" or "cooled" to the simulation temperature, T_o, by carrying out an equilibration run where the velocities of the atoms are scaled in a step-wise manner until the desired temperature, T_o, is reached. The system is further equilibrated for a specified period of time until certain properties of the system, such as average kinetic energy, remain constant. The coordinates and velocities of each atom are then obtained from the equilibrated system.

Further energy minimization routines can also be carried out. For example, a second class of methods involves calculating approximate solutions to the constrained EOM for the protein. These methods use an iterative approach to solve for the Lagrange multipliers and, typically, only need a few iterations if the corrections required are small. The most popular method of this type, SHAKE (Ryckaert et al. (1977) *J Comput Phys* 23:327; and Van Gunsteren et al. (1977) *Mol Phys* 34:1311) is easy to implement and scales as O(N) as the number of constraints increases. Therefore, the method is applicable to macromolecules such as the UBC proteins of the present invention. An alternative method, RATTLE (Anderson (1983) *J Comput Phys* 52:24) is based on the velocity version of the Verlet algorithm. Like SHAKE, RATTLE is an iterative algorithm and can be used to energy minimize the model of the subject protein.

The increasing availability of biomacromolecule structures of potential pharmacophoric molecules that have been solved crystallographically has prompted the development of a variety of direct computational methods for molecular design, in which the steric and electronic properties of substrate binding sites are use to guide the design of potential inhibitors (Cohen et al. (1990) *J. Med. Cam.* 33: 883-894; Kuntz et al. (1982) *J. Mol. Biol* 161: 269-288; DesJarlais (1988) *J. Med. Cam.* 31: 722-729; Bartlett et al. (1989) (*Spec. Publ., Roy. Soc. Chem.*) 78: 182-196; Goodford et al. (1985) *J. Med. Cam.* 28: 849-857; DesJarlais et al. *J. Med. Cam.* 29: 2149-2153). Directed methods generally fall into two categories: (1) design by analogy in which 3-D structures of known molecules (such as from a crystallographic database) are docked to the enzyme structure and scored for goodness-of-fit; and (2) *de novo* design, in which the ligand model is constructed piece-wise in the

enzyme. The latter approach, in particular, can facilitate the development of novel molecules, uniquely designed to bind to the subject human ubiquitin-conjugating enzyme.

In an illustrative embodiment, the design of potential hUbCE inhibitors begins from the general perspective of shape complimentary for the active site and substrate specificity subsites of the enzyme, and a search algorithm is employed which is capable of scanning a database of small molecules of known three-dimensional structure for candidates which fit geometrically into the target protein site. It is not expected that the molecules found in the shape search will necessarily be leads themselves, since no evaluation of chemical interaction necessarily be made during the initial search. Rather, it is anticipated that such candidates might act as the framework for further design, providing molecular skeletons to which appropriate atomic replacements can be made. Of course, the chemical complimentary of these molecules can be evaluated, but it is expected that atom types will be changed to maximize the electrostatic, hydrogen bonding, and hydrophobic interactions with the enzyme. Most algorithms of this type provide a method for finding a wide assortment of chemical structures that are complementary to the shape of a binding site of the subject enzyme. Each of a set of small molecules from a particular data-base, such as the Cambridge Crystallographic Data Bank (CCDB) (Allen et al. (1973) *J. Chem. Doc.* 13: 119), is individually docked to the binding site of the hUbCE enzyme in a number of geometrically permissible orientations with use of a docking algorithm. In a preferred embodiment, a set of computer algorithms called DOCK, can be used to characterize the shape of invaginations and grooves that form the active sites and recognition surfaces of the subject enzyme (Kuntz et al. (1982) *J. Mol. Biol* 161: 269-288). The program can also search a database of small molecules for templates whose shapes are complementary to particular binding sites of the enzyme (DesJarlais et al. (1988) *J Med Chem* 31: 722-729). These templates normally require modification to achieve good chemical and electrostatic interactions (DesJarlais et al. (1989) *ACS Symp Ser* 413: 60-69). However, the program has been shown to position accurately known cofactors for inhibitors based on shape constraints alone.

The orientations are evaluated for goodness-of-fit and the best are kept for further examination using molecular mechanics programs, such as AMBER or CHARMM. Such algorithms have previously proven successful in finding a variety of molecules that are complementary in shape to a given binding site of a receptor-enzyme, and have been shown to have several attractive features. First, such algorithms can retrieve a remarkable diversity of molecular architectures. Second, the best structures have, in previous applications to other proteins, demonstrated impressive shape complementarity over an extended surface area. Third, the overall approach appears to be quite robust with respect to small uncertainties in positioning of the candidate atoms.

Goodford (1985, *J Med Chem* 28:849-857) and Boobbyer et al. (1989, *J Med Chem* 32:1083-1094) have produced a computer program (GRID) which seeks to determine regions

of high affinity for different chemical groups (termed probes) on the molecular surface of the binding site. GRID hence provides a tool for suggesting modifications to known ligands that might enhance binding. It may be anticipated that some of the sites discerned by GRID as regions of high affinity correspond to "pharmacophoric patterns" determined inferentially from a series of known ligands. As used herein, a pharmacophoric pattern is a geometric arrangement of features of the anticipated ligand that is believed to be important for binding. Attempts have been made to use pharmacophoric patterns as a search screen for novel ligands (Jakes et al. (1987) *J Mol Graph* 5:41-48; Brint et al. (1987) *J Mol Graph* 5:49-56; Jakes et al. (1986) *J Mol Graph* 4:12-20); however, the constraint of steric and "chemical" fit in the putative (and possibly unknown) receptor binding site is ignored. Goodsell and Olson (1990, *Proteins: Struct Funct Genet* 8:195-202) have used the Metropolis (simulated annealing) algorithm to dock a single known ligand into a target protein. They allow torsional flexibility in the ligand and use GRID interaction energy maps as rapid lookup tables for computing approximate interaction energies. Given the large number of degrees of freedom available to the ligand, the Metropolis algorithm is time-consuming and is unsuited to searching a candidate database of a few thousand small molecules.

Yet a further embodiment of the present invention utilizes a computer algorithm such as CLIX which searches such databases as CCDB for small molecules which can be oriented in the receptor binding site in a way that is both sterically acceptable and has a high likelihood of achieving favorable chemical interactions between the candidate molecule and the surrounding amino acid residues. The method is based on characterizing the receptor site in terms of an ensemble of favorable binding positions for different chemical groups and then searching for orientations of the candidate molecules that cause maximum spatial coincidence of individual candidate chemical groups with members of the ensemble. The current availability of computer power dictates that a computer-based search for novel ligands follows a breadth-first strategy. A breadth-first strategy aims to reduce progressively the size of the potential candidate search space by the application of increasingly stringent criteria, as opposed to a depth-first strategy wherein a maximally detailed analysis of one candidate is performed before proceeding to the next. CLIX conforms to this strategy in that its analysis of binding is rudimentary -it seeks to satisfy the necessary conditions of steric fit and of having individual groups in "correct" places for bonding, without imposing the sufficient condition that favorable bonding interactions actually occur. A ranked "shortlist" of molecules, in their favored orientations, is produced which can then be examined on a molecule-by-molecule basis, using computer graphics and more sophisticated molecular modeling techniques. CLIX is also capable of suggesting changes to the substituent chemical groups of the candidate molecules that might enhance binding.

The algorithmic details of CLIX is described in Lawerence et al. (1992) *Proteins* 12:31-41, and the CLIX algorithm can be summarized as follows. The GRID program is

used to determine discrete favorable interaction positions (termed target sites) in the binding site of the protein for a wide variety of representative chemical groups. For each candidate ligand in the CCDB an exhaustive attempt is made to make coincident, in a spatial sense in the binding site of the protein, a pair of the candidate's substituent chemical groups with a pair of corresponding favorable interaction sites proposed by GRID. All possible combinations of pairs of ligand groups with pairs of GRID sites are considered during this procedure. Upon locating such coincidence, the program rotates the candidate ligand about the two pairs of groups and checks for steric hindrance and coincidence of other candidate atomic groups with appropriate target sites. Particular candidate/orientation combinations that are good geometric fits in the binding site and show sufficient coincidence of atomic groups with GRID sites are retained.

Consistent with the breadth-first strategy, this approach involves simplifying assumptions. Rigid protein and small molecule geometry is maintained throughout. As a first approximation rigid geometry is acceptable as the energy minimized coordinates of the hUbCE deduced structure, as described in Example 9, describe an energy minimum for the molecule, albeit a local one. If the surface residues of the site of interest are not involved in crystal contacts then the crystal configuration of those residues. We believe that the deduced structure described in Example 9 should reasonably mimic the mean solution configuration. Moreover, the equivalent models of caUbCE, spUbCE, and rapUBC can be derived by the same method.

A further assumption implicit in CLIX is that the potential ligand, when introduced into the binding site of ubiquitin-conjugating enzyme, does not induce change in the protein's stereochemistry or partial charge distribution and so alter the basis on which the GRID interaction energy maps were computed. It must also be stressed that the interaction sites predicted by GRID are used in a positional and type sense only, i.e., when a candidate atomic group is placed at a site predicted as favorable by GRID, no check is made to ensure that the bond geometry, the state of protonation, or the partial charge distribution favors a strong interaction between the protein and that group. Such detailed analysis should form part of more advanced modeling of candidates identified in the CLIX shortlist.

Yet another embodiment of a computer-assisted molecular design method for identifying inhibitors of the subject ubiquitin-conjugating enzyme comprises the *de novo* synthesis of potential inhibitors by algorithmic connection of small molecular fragments that will exhibit the desired structural and electrostatic complementarity with the active site of the enzyme. The methodology employs a large template set of small molecules with are iteratively pieced together in a model of the UBC active site. Each stage of ligand growth is evaluated according to a molecular mechanics-based energy function, which considers van der Waals and coulombic interactions, internal strain energy of the lengthening ligand, and

desolvation of both ligand and enzyme. The search space can be managed by use of a data tree which is kept under control by pruning according to the binding criteria.

In an illustrative embodiment, the search space is limited to consider only amino acids and amino acid analogs as the molecular building blocks. Such a methodology generally employs a large template set of amino acid conformations, though need not be restricted to just the 20 natural amino acids, as it can easily be extended to include other related fragments of interest to the medicinal chemist, e.g. amino acid analogs. The putative ligands that result from this construction method are peptides and peptide-like compounds rather than the small organic molecules that are typically the goal of drug design research. The appeal of the peptide building approach is not that peptides are preferable to organics as potential pharmaceutical agents, but rather that: (1) they can be generated relatively rapidly de novo; (2) their energetics can be studied by well-parameterized force field methods; (3) they are much easier to synthesize than are most organics; and (4) they can be used in a variety of ways, for peptidomimetic inhibitor design, protein-protein binding studies, and even as shape templates in the more commonly used 3D organic database search approach described above.

Such a *de novo* peptide design method has been incorporated in a software package called GROW (Moon et al. (1991) *Proteins* 11:314-328). In a typical design session, standard interactive graphical modeling methods are employed to define the structural environment in which GROW is to operate. For instance, environment could be the active site cleft of hUbCE or rapUBC, or it could be a set of features on the protein's surface to which the user wishes to bind a peptide-like molecule, e.g. a ubiquitin, p53, E6 or E6AP mimetic. The GROW program then operates to generate a set of potential ligand molecules. Interactive modeling methods then come into play again, for examination of the resulting molecules, and for selection of one or more of them for further refinement.

To illustrate, GROW operates on an atomic coordinate file generated by the user in the interactive modeling session, such as the coordinates provided in Figure 1, or the coordinates of the active site provided in Figure 3, plus a small fragment (e.g., an acetyl group) positioned in the active site to provide a starting point for peptide growth. These are referred to as "site" atoms and "seed" atoms, respectively. A second file provided by the user contains a number of control parameters to guide the peptide growth (Moon et al. (1991) *Proteins* 11:314-328).

The operation of the GROW algorithm is conceptually fairly simple, and is summarized in Figure 4. GROW proceeds in an iterative fashion, to systematically attach to the seed fragment each amino acid template in a large preconstructed library of amino acid conformations. When a template has been attached, it is scored for goodness-of-fit to the receptor site, and then the next template in the library is attached to the seed. After all the templates have been tested, only the highest scoring ones are retained for the next level of growth. This procedure is repeated for the second growth level; each library template is

attached in turn to each of the bonded seed/amino acid molecules that were retained from the first step, and is then scored. Again, only the best of the bonded seed/dipeptide molecules that result are retained for the third level of growth. The growth of peptides can proceed in the N-to-C direction only, the reverse direction only, or in alternating directions, depending on the initial control specifications supplied by the user. Successive growth levels therefore generate peptides that are lengthened by one residue. The procedure terminates when the user-defined peptide length has been reached, at which point the user can select from the constructed peptides those to be studied further. The resulting data provided by the GROW procedure include not only residue sequences and scores, but also atomic coordinates of the peptides, related directly to the coordinate system of the receptor site atoms.

In yet another embodiment, potential pharmacophoric compounds can be determined using a method based on an energy minimization-quenched molecular dynamics algorithm for determining energetically favorable positions of functional groups in the binding cites of the subject ubiquitin-conjugating enzyme. The method can aid in the design of molecules that incorporate such functional groups by modification of known ligands or *de novo* construction.

For example, the multiple copy simultaneous search method (MCSS) described by Miranker et al. (1991) *Proteins* 11: 29-34. To determine and characterize a local minima of a functional group in the forcefield of the protein, multiple copies of selected functional groups are first distributed in a binding site of interest on the UBC protein. Energy minimization of these copies by molecular mechanics or quenched dynamics yields the distinct local minima. The neighborhood of these minima can then be explored by a grid search or by constrained minimization. In one embodiment, the MCSS method uses the classical time dependent Hartee (TDH) approximation to simultaneously minimize or quench many identical groups in the forcefield of the protein.

Implementation of the MCSS algorithm requires a choice of functional groups and a molecular mechanics model for each of them. Groups must be simple enough to be easily characterized and manipulated (3-6 atoms, few or no dihedral degrees of freedom), yet complex enough to approximate the steric and electrostatic interactions that the functional group would have in binding to the site of interest in the UBC protein. A preferred set is, for example, one in which most organic molecules can be described as a collection of such groups (*Patai's Guide to the Chemistry of Functional Groups*, ed. S. Patai (New York: John Wiley, and Sons, (1989)). This includes fragments such as acetonitrile, methanol, acetate, methyl ammonium, dimethyl ether, methane, and acetaldehyde.

Determination of the local energy minima in the binding site requires that many starting positions be sampled. This can be achieved by distributing, for example, 1,000-5,000 groups at random inside a sphere centered on the binding site; only the space not occupied by the protein needs to be considered. If the interaction energy of a particular group at a

certain location with the protein is more positive than a given cut-off (e.g. 5.0 kcal/mole) the group is discarded from that site. Given the set of starting positions, all the fragments are minimized simultaneously by use of the TDH approximation (Elber et al. (1990) *J Am Chem Soc* 112: 9161-9175). In this method, the forces on each fragment consist of its internal forces and those due to the protein. The essential element of this method is that the interactions between the fragments are omitted and the forces on the protein are normalized to those due to a single fragment. In this way simultaneous minimization or dynamics of any number of functional groups in the field of a single protein can be performed.

Minimization is performed successively on subsets of, e.g. 100, of the randomly placed groups. After a certain number of step intervals, such as 1,000 intervals, the results can be examined to eliminate groups converging to the same minimum. This process is repeated until minimization is complete (e.g. RMS gradient of 0.01 kcal/mole/Å). Thus the resulting energy minimized set of molecules comprises what amounts to a set of disconnected fragments in three dimensions representing potential pharmacophores.

The next step then is to connect the pharmacophoric pieces with spacers assembled from small chemical entities (atoms, chains, or ring moieties). In a preferred embodiment, each of the disconnected can be linked in space to generate a single molecule using such computer programs as, for example, NEWLEAD (Tschinke et al. (1993) *J Med Chem* 36: 3863,3870). The procedure adopted by NEWLEAD executes the following sequence of commands (1) connect two isolated moieties, (2) retain the intermediate solutions for further processing, (3) repeat the above steps for each of the intermediate solutions until no disconnected units are found, and (4) output the final solutions, each of which is single molecule. Such a program can use for example, three types of spacers: library spacers, single-atom spacers, and fuse-ring spacers. The library spacers are optimized structures of small molecules such as ethylene, benzene and methylamide. The output produced by programs such as NEWLEAD consist of a set of molecules containing the original fragments now connected by spacers. The atoms belonging to the input fragments maintain their original orientations in space. The molecules are chemically plausible because of the simple makeup of the spacers and functional groups, and energetically acceptable because of the rejection of solutions with van-der Waals radii violations.

In one embodiment of the invention, the target regulatory protein is the tumor suppressor p53, and any one of the above assays or molecular modeling protocols is used to identify inhibitors of ubiquitin-mediated destruction of p53, such as by disrupting interaction of hUbCE or rapUBC with p53, or interactions between hUbCE or rapUBC and other proteins of the ubiquitin system such as E6 or E6AP, or alternatively, by mechanistically inhibiting the enzymatic activity of the enzyme. Many lines of evidence point to the importance of p53 in human carcinogenesis. For instance, mutations within the p53 gene are the most frequent genetic aberration thus far associated with human cancer. Although p53

can block the progression of the cell cycle when artificially expressed at high levels, it appears to be dispensable for normal development. Thus, for mice containing homozygous deletions and humans harboring germline mutations of p53, development is normal and p53 protein is expressed at very low levels in most cell types. Emerging evidence, however, suggests that p53 is a checkpoint protein that plays an important role in sensing DNA damage or regulating cellular response to stress. Under normal conditions, p53 is an unstable protein and is present at very low levels in the cell, and the level of p53 in a cell appears to be controlled at least in party by degradation involving the ubiquitin system and, based on data presented herein, is likely to be mediated by the subject hUbCE or rapUBC. Treating cells with UV light or X rays dramatically reduces the rate of p53 degradation, leading to a rapid increase in its concentration in the cell and presumably inducing the transcription of genes that block passage through the restriction point. However, while normal cell lines irradiated in G_1 fail to enter S phase, many tumor lines do not. In fact, there is a perfect correlation between cell lines that lack this feedback control and cells that have mutations in the p53 gene. These mutations are of two sorts: recessive mutations that inactivate the gene, and dominant mutations that produce abnormal proteins. An inhibitor developed using the subject hUbCE or rapUBC in a ubiquitin-conjugating assay or by rational drug design could subsequently be used therapeutically to enhance the function of the p53 checkpoint by increasing the steady state concentration of p53 in the treated cell. Given that elevated levels of wild-type p53 protein can lead to apoptosis in a variety of transformed cell types (Yonish-Rouach et al. (1991) *Nature* 352:345-347; Shaw et al. *PNAS* 89:4495-4499; and Caelles et al. (1994) *Nature* 370:220-223), inhibitors of hUbCE or rapUBC-mediated degradation of p53 may be attractive therapeutic agents not only in cervical cancer, but also other cancer types, by increasing the fortitude of the checkpoint in transformed cells which contain wild-type p53, or by offsetting a diminishment in p53 activity by increasing the level of (mutant) p53. Moreover, such agents can also be used prophylactically in normal cells to increase p53 levels and thereby enhance the protection against DNA damaging agents when it is known that exposure to damaging agents, such as radiation, is imminent.

Moreover, the oncogenic activity of certain viruses, such as the simian virus 40 (SV40), the adenovirus type 5 (Ad5), and the high human papilloma virus types 16 and 18 (HPV16 and HPV18), has been correlated with the virus' ability to interact with and inactivate the cellular p53 protein. In the instance of the high-risk papilloma viruses, the association of the viral oncoprotein E6 with p53 leads to the specific ubiquitination and degradation of p53. This has suggested a model in which E6 immortalizes cells by deregulating cell growth control through the elimination of the p53 tumor suppressor protein. This models accounts for the observations that p53 levels are very low in HPV-immortalized cells and that the half-life of p53 in HPV16-immortalized keratinocytes is shorter than in primary keratinocytes. Thus, the present invention can be employed in the identification of an agent that can block

the ubiquitin dependent degradation of p53 as mediated by E6, and thereby block proliferation of HPV-transformed cells.

The subject human ubiquitin conjugating enzyme is likely to be involved in altering the activity of other cellular proteins, particularly proteins which seem to have short half-lives, and the present invention contemplates the use of hUbCE or rapUBC inhibitors, including antagonistic forms of the hUbCE or rapUBC protein, to inhibit the ubiquitination of other cellular proteins by hUbCE or rapUBC. For example, in another embodiment, the regulatory protein ubiquitinated by hUbCE or rapUBC is the *myc* oncoprotein. The *myc* regulatory protein is activated by translocation or mutation in many B-cell lymphomas or by amplification in tumor types, such as small cell lung cancer and breast cancer. The *c-myc* gene is the cellular homolog of the viral oncogene v-myc, which is found in a number of avian and feline retroviruses which induce leukemia and carcinomas. *Myc* has been implicated in the control of normal cell proliferation by many studies. In particular, it is one of the immediate early growth response genes that are rapidly induced in quiescent cells upon mitogenic induction, suggesting that it plays some role in mediating the transition from quiescence to proliferation. However, increased levels of *myc* itself is not sufficient to cause proliferation. In fact, in normal cells the opposite happens and the cell undergoes apoptosis. Therefore, inhibitors identified in the present assay can be used to effectively induce apoptosis in cells which do not normally overexpress *myc*. For example, specific delivery of these agents to lymphocytes can be used to inhibit proliferation of B- and/or T-cells in order to induce clonal deletion and generate tolerance to particular antigens.

In tumor cells, on the other hand, elevated or deregulated expression of *c-myc* is so widespread as to suggest a critical role for *myc* gene activation in multi-stage carcinomas (Field et all. (1990) *Anticancer Res* 10:1-22; and Spencer et al. (1991) *Adv Cancer Res* 56:1-48). However, such overexpression of *myc* in these cells is typically believed to be accompanied by expression of other cellular proteins, such as *bcl-2*. Interestingly, however, almost all tumor cells tested that overexpress *myc* readily undergo apoptosis in the presence of cytotoxic and growth-inhibitory drugs (Cotter et al. (1990) *Anticancer Res* 10:1153-1159; and Lennon et al. (1990) *Biochem Soc Trans* 18:343-345). Therefore, inhibitors of the ubiquitin-mediated degradation of *myc* can be used to further deregulate the expression of *myc* in order to render the cells even more sensitive to a chemotherapeutic treatment, or to possibly upset the careful balance of the transformed cell and cause apoptosis to occur even in the absence of a second cytotoxic drug.

The regulation of cyclin by ubiquitination is yet another therapeutic target which may implicate hUbCE or rapUBC inhibitors. Cyclin degradation is a key step governing exit from mitosis and progression into the next cell-cycle. For example, the transition from metaphase to anaphase which marks the end of mitosis in induced by the degradation of cyclin by a ubiquitin-mediated pathway, which in turn leads to the inactivation of cyclin-dependent

kinases (cdk) operational at that cycle-cycle stage. As cells enter interphase, cyclin degradation ceases, cyclin accumulates and, as a result of a complex series of post-translational modifications, cyclin /cdk complexes are activated as kinases which drive the cell through mitosis. Cyclin degradation is thus one of the crucial events in exiting mitosis. Indeed, cyclin mutants that retain the ability to activate the cdk complexes, but which cannot be degraded, arrest the cell-cycle in mitosis. Similar cyclin-dependence exists at other points of the cell-cycle as well. Thus, inhibitors of ubiquitin-mediated degradation of a cyclin (such as where the cyclin is chosen from cyclin A, B, C, D1, D2, D3, E or F) can be used as antiproliterative agents.

Yet another candidate substrate of for E2 enzymes is the cyclin-dependent kinase inhibitor $p27^{kip1}$ (Polyak et al. (1994) *Cell* 78:59-66; and Toyoshima et al. (1994) *Cell* 78:67-74). This protein has been implicated in G_1 phase arrest, such as mediated by TGF-β and cell-cell contact. As described in the appended examples, we have found that ubiquitin conjugating enzymes are able to ubiquitinate p27, indicating that cellular turnover of that protein is dependent at least in part on ubiquitin-mediated destruction. Consequently, inhibition of ubiquitin transfer to p27 may result in accumulation of this cell-cycle inhibitor. An agent which inhibits the E2-mediated degradation of p27 would therefore be a cytostatic agent.

Such cytostatic agents would be useful for inhibiting proliferation of both normal and transformed cells. For example, an inhibitor of E2-mediated ubquitination of p27 could be used to prevent proliferation of lymphocytes, much the same as rapamycin and the like, and could be used as an immunosuppressant. Likewise, accumulation of p27 in fibroblasts could be used as part of a therapy for the treatment of a connective tissue disorder, or for controlling would healing processes.

P27 modulating agents may also be used for the treatment of hyperplastic epidermal conditions, such as psoriasis, as well as for the treatment of neoplastic epidermal conditions such as those characterized by a high proliferization rate for various skin cancers, as for example basal cell carcinoma and squamous cell carcinoma.

Normal cell proliferation is generally marked by responsiveness to negative autocrine or paracrine growth regulators, such as members of the TGF-β family, e.g. TGF-β1, TGF-β2 or TGF-β3, and related polypeptide growth inhibitors, e.g. activins, inhibins, Müllerian inhibiting substance, decapentaplegic, bone morphogenic factors, and vg1 (e.g. terminal differentiation inducers). Ordinarily, control of cellular proliferation by such growth regulators, particularly in epithelial and hemopoietic cells, is in the form of growth inhibition with p27 accumulation being associated with at least TGF-β response. This is generally accompanied by differentiation of the cell to a post-mitotic phenotype. However, it has been observed that a significant percentage of human cancers derived from these cells types display a reduced responsiveness to growth regulators such as TGF-β. For instance, some

tumors of colorectal, liver epithelial, and epidermal origin show reduced sensitivity and resistance to the growth-inhibitory effects of TGF-β as compared to their normal counterparts. Treatment of such tumors with antagonists of ubiquitination of p27 provides an opportunity to restore the function of a TGF-β mediated checkpoint.

The subject E2 inhibitors can also be used in the treatment of hyperproliferative vascular disorders, e.g. smooth muscle hyperplasia (such as atherosclerosis) or restinosis, as well as other disorders characterized by fibrosis, e.g. rheumatoid arthritis, insulin dependent diabetes mellitus, glomerulonephritis, cirrhosis, and scleroderma, particularly proliferative disorders in which loss of TGF-β autocrine or paracrine signaling is implicated. For example, restinosis continues to limit the efficacy of coronary angioplasty despite various mechanical and pharmaceutical interventions that have been employed. An important mechanism involved in normal control of intimal proliferation of smooth muscle cells appears to be the induction of autocrine and paracrine TGF-β inhibitory loops in the smooth muscle cells (Scott-Burden et al. (1994) *Tex Heart Inst J* 21:91-97; Graiger et al. (1993) *Cardiovasc Res* 27:2238-2247; and Grainger et al. (1993) *Biochem J* 294:109-112). Loss of sensitivity to TGF-β, or alternatively, the overriding of this inhibitory stimulus such as by PDGF autostimulation, can be a contributory factor to abnormal smooth muscle proliferation in restinosis. It may therefore be possible to treat or prevent restinosis by the use of agents which inhibit ubiquitination of p27, thereby causing its accumulation.

Yet a further possible substrate of the subject hUbCE or rapUBC is the *fos* oncogene product, which can undergo ubiquitin-mediated degradation in a cell and has been implicated in neoplastic transformation as well as in mediating the action of a variety of extracellular stimuli. The control of gene expression by c-fos is believed to play a critical role in cellular proliferation and developmental responses, and alterations in the normal pattern of c-fos can lead to oncogenesis. Given the prominence of c-fos as an early response gene, apparent over-expression and prolonged lifetime of c-fos, as may be caused by an inhibitor of the ubiquitin-mediated degradation of c-fos, might sufficiently unbalance the cell-cycle and cause cell death. Alternatively, such inhibitors can be used to mimic the effects of an external stimulus on the cell, such as treatment with a cytokine.

Exemplification

The invention now being generally described, it will be more readily understood by reference to the following examples which are included merely for purposes of illustration of certain aspects and embodiments of the present invention, and are not intended to limit the invention.

We have defined the biochemical roles of hUbCE and E6AP in the E6 stimulated ubiquitination of p53 *in vitro* and have shown that inhibition of these enzymes *in vivo* can lead to an inhibition of E6-stimulated p53 degradation. As described in the examples below,

inhibition of hUbCE and E6AP enzyme function *in vivo* causes an inhibition of E6-stimulated p53 degradation. The level of inhibition achieved in the micro-injection experiments in Example 8 was 25-30%. This may be a consequence of not every injected cell achieving high level expression of the injected construct, a phenomenon we have noted before in many different systems. It may also suggest that there is some redundancy in the cellular ubiquitin conjugation machinery, or that the intracellular concentrations of E1, hUbCE and E6AP are not rate-limiting for p53 degradation in the cell line used. All of our data suggest that E6 is absolutely required for ubiquitination of p53 in our *in vitro* and *in vivo* assay systems. We are currently investigating the possibility that hUbCE and E6AP are involved in the normal turnover of p53, with the possible involvement of an, as yet, unidentified cellular E6 homolog.

Example 1

Cloning and Expression of a Novel Human Ubiquitin-conjugating Enzyme

The cDNA encoding the human ubiquitin-conjugating enzyme of the present invention was cloned from HeLa cells (ATCC CCL2). Briefly, polyadenylated RNA was isolated from cultured HeLa cells and first strand cDNA was prepared following standard protocols (c.f., Chomczynski U.S. Patent No. 4,843,155; and Sambrook et al. *Molecular Cloning: A Laboratory Manual*, CSHL Press, Cold Spring Harbor, NY (1989)). Using the nested PCR primer sets 5'-$(GC)_3$AAGCTTTAYGARGGWGGWGTYTTYTT-3' (SEQ ID No. 8), 5'-$(GC)_3$GAATTCACNGCRTAYTTYTTNGTCCCAYTC-3' (SEQ ID No. 9) and 5'-$(GC)_3$AAGCTTCCNGTNGGNG-AYTTRTTYCAYTGGCA-3' (SEQ ID No. 10), 5-$(GC)_3$G-AATTCATNGTNARNGCNGGCGACCA-3' (SEQ ID No. 11), which also provided convenient restriction sites in the PCR products, the coding sequences for the hUbCE gene was amplified from the HeLa cDNA library, and a HindIII-EcoRI fragment therefrom was subsequently ligated into a pBluescript II KS+ phagemid (pKS+ Stratagene catalog no. 212207) for further manipulation. The resulting pKS-hUbCE construct was amplified in XL1-Blue Cells (Strategene Catalog no. 260268), and double stranded construct purified. The nucleic acid sequence determined for the hUbCE clone is represented in SEQ ID NO. 1, and the corresponding deduced amino acid sequence is provided in SEQ ID No. 2.

The hUbCE gene was subsequently sub-cloned from pKS+ into other expression vectors to generate gene constructs for producing the recombinant hUbCE protein in either bacterial or insect cells. In some instances, the recombinant hUbCE was provided with exogenous sequences to produce fusion proteins, where the additional sequences of the fusion protein facilitate its purification. For example, after further amplification, the pKS-E2 construct was cut with XhoI and EcoRI, and the fragment containing the hUbCE coding sequence sub-cloned into a pGEX vector (Pharmacia catalog no. PGEX-4T) previously digested with SalI and EcoRI. The resulting pGEX-hUbCE construct encoded a glutathione-

S-transferase (GST)/hUbCE fusion (Smith et al. (1988) *Gene* 67:31-40). The pGEX construct was introduced into *E.coli* by transformation, and the transformants grown in liquid media (LB) in the presence of IPTG. Purification of GST/hUbCE fusion protein was by standard protocols (*Current Protocols in Molecular Biology*, eds. Ausubel et al. (NY:John Wiley & Sons, 1991); Pharmacia instruction booklet (for catalog no. 27-4570)) using a glutathione-sepharose column (Pharmacia catalog no. 27-4570). Treatment with thrombin removed the GST domain from the fusion protein.

Alternatively, the hUbCE coding sequence was excised from the pKS-hUbCE construct as a HindIII-EcoRI fragment and ligated into pVL1393 cut with Sma I and Eco I. Briefly, the hUbCE gene fragment was purified by agarose gel separation, and ligated into the baculorvirus vector pVL1393 (Invitrogen catalog no. V1392-20) previously cut with Sma I and Bgl II. The pVL1393-hUbCE construct was then used to transfect spodoptera frugiperda (Sf9 cells, ATCC CRL 1711), and the cells maintained in insect cell culture media (Grace's Antheraea medium) supplemented with 10% FBS, lactal bumin hydrolysate, TC yeastolate and glutamate (Invitrogen catalog no. B823) following standard protocols (Invitrogen product guide; Summers and Smith (1987); *Texas Agricultural Experiment Station Bulletin No. 1555*, College Station, Texas; Luckow et al. (1988) *Bio/technology* 6:47-55; and Miller et al., in *Genetic Engineering, Vol. 8* ed. Setlow and Hollaender (Plenum Press: New York) pages 277-298) . Transfected cells are grown until cells begin to lose their adherence to the culture plate surface, at which time the cells are harvested, collected by centrifugation, and lysed. The lysate is clarified by centrifugation to remove the cell wall debris, and the hUbCE can be purified from the lysate.

For instance, the hUbCE protein was isolated on an E1:ubiquitin charged column. Isolation of enzymes of the ubiquitin-conjugating system has been greatly assisted by "covalent" ubiquitin-affinity chromatography (Crechanover et al. (1982) *J. Biol. Chem.* 257:2537-2542; and Pickart et al. (1985) *J. Biol. Chem.* 260:1573-1581). This method takes advantage of the fact that the E1 enzyme is capable of forming a thiol ester with immobilized ubiquitin (e.g. ubiquitin-Sepharose) in the presence of ATP. Moreover, E1 enzymes bound to the immobilized ubiquitin can be exchanged with the subject hUbCE protein. Thus, both E1 and the subject hUbCE protein can be specifically purified on such columns, and can be recovered after elution with, for example, dithiothreitol. Moreover, with minor changes, this protocol can be used to isolate hUbCE:Ub conjugates (e.g. activated ubiquitin conjugates) for use in therapeutic target assays.

As described in U.S. patent application 08/176,937, the an E1-containing lysate was applied to a sepharose-ubiquitin column (Hershko et al. (1983) *J. Biol. Chem.* 257:2537-2542) in the presence of ATP (e.g. 5mM ATP, 10mM $MgCl_2$, and 0.2 mM dithiothreitol, 50mM Tris-HCl (pH 7.2)). The column was washed several times with this buffer. A clarified lysate of the hUbCE -producing insect cells, adjusted to 50mM Tris-HCl (pH 7.2),

5mM ATP, 10mM $MgCl_2$, and 0.2 mM dithiothreitol, was then applied to the Ub:E1 column, washed, then eluted to remove any remaining ub:E1 (e.g. hUbCE will be exchanged for E1 on the column). The subject hUbCE protein was then eluted from the column by washing with 50mM Tris-HCl (pH 9.0) containing 2mM dithiothreitol.

In another exemplary embodiment, the recombinant hUbCE protein is generated as a poly(His) fusion protein for purification on a Ni^{2+} metal column. An XhoI to EcoRI fragment of the pKS construct is cloned into the pBlueBac A baculovirus (Intvitrogen catalog no. V360-20) previously digested with XhoI and EcoRI. Following the manufacturer's protocols, the His_6-hUbCE fusion protein is then expressed in Sf9 insect cells, and purified on a Ni^{2+} charged sepharose resin (Invitrogen catalog no. R801; see also Hochuli et al. (1987) *J. Chromatography* 411:177-184; and Janknecht et al. (1991) *PNAS* 88:8972-8976). Following purification of the fusion protein, the His_6 tag can be removed by treatment with entrokinase.

Example 2

Isolation of components of an in vitro ubiquitin conjugating system

Ubiquitin was obtained from commercial sources, and the remaining protein components of the reconstituted protein system were cloned from HeLa cells (ATCC CCL2). Briefly, polyadenylated RNA was isolated from cultured HeLa cells and first strand cDNA was prepared following standard protocols (c.f., Chomczynski U.S. Patent No. 4,843,155; and Sambrook et al. *Molecular Cloning: A Laboratory Manual*, CSHL Press, Cold Spring Harbor, NY (1989)). PCR primers, designed to amplify DNA sequences encoding each of the component proteins, as well as provide convenient restriction sites to the PCR products, were used to isolate coding sequences for a human E1, human p53, HPV-18 E6, human E6-AP, and various human E2's, which were subsequently ligated into a pBluescript II KS+ phagemid (pKS+ Stratagene catalog no. 212207) for further manipulation. As described below, each of the component proteins genes were subsequently sub-cloned from pKS+ into other expression vectors to generate gene constructs for producing the recombinant proteins in either bacterial or insect cells. In some instances, the recombinant proteins have been provided with exogenous sequences to produce fusion proteins, where the additional sequences of the fusion protein facilitate its purification.

i) Human E1

Utilizing the primers 5'-$(GC)_3$AAGCTTATGTCCAGCTCGCCGCTGTCCAAG-3' and 5'-$(GC)_3$GGATCCTCAGCGGATGGTGTATCGGACATA-3'. The coding sequence for a human E1 (SEQ ID No. 14) was amplified from a HeLa cell cDNA library. The PCR amplification product containing the E1 coding sequences was purified and cut with Hind III and Bam HI (restriction sites provided by the PCR primers), and ligated into the pKS+

phagemid. The resulting pKS-E1 construct was amplified in XL1-Blue Cells (Strategen catalog no. 260268), and double stranded construct purified.

A Hind III/ fill to BamHI fragments containing the E1 coding sequence was isolated from the pKS-E1 construct, where "Hind III/ fill" indicates that a Hind III overhand generated in the fragment has been filled to form a blunt-end using Klenow and dNTPs. The E1 gene fragment was purified by agarose gel separation, and ligated into the baculorvirus vector pVL1393 (Invitrogen catalog no. V1392-20) previously cut with Sma I and Bgl II. The pVL1393-E1 construct was used to transfect spodoptera frugiperda (Sf9) cells) (ATCC CRL 1711), and the cells maintained in insect cell culture media (Grace's Antheraea medium) supplemented with 10% FBS, lactal bumin hydrolysate, TC yeastolate and glutamate (Invitrogen catalog no. B823) following standard protocols (Invitrogen product guide; Summers and Smith (1987); *Texas Agricultural Experiment Station Bulletin No. 1555*, College Station, Texas; Luckow et al. (1988) Bio/technology 6:47-55; and Miller et al., in *Genetic Engineering, Vol. 8* (Setlow and Hollaender, eds) pp. 277-298, Plenum, New York). Transfected cells are grown until cells begin to lose their adherence to the culture plate surface, at which time the cells are harvested, collected by centrifugation, and lysed. The lysate is clarified by centrifugation to remove the cell wall debris, and the E1 containing lysate is applied to a sepharose-ubiquitin column (Hershko et al. (1983) *J. Biol. Chem.* 257:2537-2542) in the presence of ATP (e.g. 5m MATP, 10mM $MgCl_2$, and 0.2 mM clithiothreitol, 50mM Tris-HCl (pH 7.2)). The column is washed several times with this buffer, and the E1 protein eluted with the following solutions: 1M KCl containing 50mM Tris-HCl, pH7.2 (KCl eluate); the above Tris buffer, to remove salt; and finally 2mM ATP and 0.04 mM sodium pyrophosphate in the above Tri buffer. The E1-containing eluate can be concentrated, as well as placed in new buffer solution, by centrifuge ultrafiltration with CentriPrep or Centricon membranes (Amicon Corp., MA). Alternatively, the ubiquitin-immoblized E1 can be used, as described below, in the purification of E2 enzymes.

ii) Human E2

A human rad6 homolog (SEG ID No. 15) was amplified from the HeLa cel cDNA using the primers 5'-$(GC)_3$AAGCTTATGTCGACCCCGGCCCGGAGGAGG-3' and 5'-$(GC)_3$GAATTCTTATGAATCATTCCAGCTTTGTTC-3' and cloned into pBluescript II pKS+ as a Hind III-EcoRI fragment. After further amplification, the pKS-E2 construct was cut with XhoI and NotI, and the fragment containing E2 coding sequence sub-cloned into a pGEX vector (Pharmacia catalog no. PGEX-4T-3) previously digested with SalI and NotI. The resulting pGEX-E2 construct encoded a glutathione-S-transferase (GST)/E2 fusion (Smith et al. (1988) *Gene* 67:31-40). The pGEX construct was introduced into *E.coli* by transfromation, and the transformants grown in liquid media (LB) in the presence of IPTG. Purification of GST/E2 fusion protein was by standard protocols (*Current Protocols in*

Molecular Biology, eds. Ausubel et al. (NY:John Wiley & Sons, 1991); Pharmacia instruction booklet (for catalog no. 27-4570)) using a glutathione-sepharose column (Pharmacia catalog no. 27-4570). Treatment with thrombin removed the GST domain from the fusion protein.

Alternatively, the rad6 coding sequence was excised from the pKS-rad6 construct as a HindIII-EcoRI fragment and ligated into pVL1393 cut with Sma I and Eco I. The E2 protein is produced in Sf9 cells, as described above, and purified on a sepharose-uibiquitin:E1 column. As above, a clarified lysate of the E2-producing insect cells, adjusted to 50mM Tris-HCl (pH 7.2), 5mM ATP, 10mM $MgCl_2$, and 0.2 mM dithiothreitol, is applied to the ub:E1 column, washed, then eluted to remove any remaining ub:E1 (e.g. E2 will be exchanged for E1 on the column). Rad6 is then eluted from the column by washing with 50mM Tris-HCl (pH 9.0) containing 2mM dithiothreitol.

In similar fashion, recombinant forms of human UBC3/CDC34 (SEQ ID No. 19) were produced.

iii) HPV-18 E6

The coding-sequence for HPV-18 E6 (SEQ. ID No. 16) was amplified from the HeLa cell cDNA library using the primers 5'-$(GC)_3$AAGCTTATGGCGCGCTTTGAG-GATCCAACA-3' and 5'-$(GC)_3$GAATTCTTATACTTGTGTTTCTCTGCGTCG-3', the PCR products purified, and the amplified E6 sequences digested with Hind III and EcoRI and ligated into a pBlueScript II pKS+ phagemid. Several different expression vectors were generated by subcloning the E6 sequences from the pKS-E6 construct. For example, a Hind III to EcoRI fragment containing E6 coding sequences was ligated into pVL1393 cut with Sma I and EcoRI to produce baculovirus expression system as described above.

Alternatively, E6 has been generated as His_6 fusion protein for purification on a Ni^{2+} metal column. An XhoI to EcoRI fragment of the pKS construct was cloned into the pBlueBac A baculovirus (intvitrogen catalog no. V360-20) previously digested with XhoI and EcoRI. Following the manufacturer's protocols, the His_6-E6 fusion protein was expressed in Sf9 insect cells, and purified on a Ni^{2+} charged sepharose resin (Invitrogen catalog no. R801; sell also Hochuli et al. (1987) *J. Chromatography* 411:177-184; and Janknecht et al. (1991) *PNAS* 88:8972-8976). Following purification of the fusion protein, the His_6 tag can be removed by treatment with entrokinase.

iv) Human E6-AP

E6-AP (SEQ ID No. 17) was cloned from the HeLa cell cDNA library using the PCR primers 5'-$(GC)_3$AAGCTTTCAGGACCTCAGTCTGACGAC-3' and 5'$(GC)_3$ GGATCCTTACAGCATGCCAAATCCTTTGGC-3', wherein the amplified E6-AP sequences were digested with Hind III and Bam HI and ligated into pBluescript II pkst.

Constructs for expressing both HIS_6 tagged and GST tagged versions of E6-AP were generated. In one instance, an NheI to BamHI E6-AP containing fragment was cloned into pBlueBacA (cut with NheI and BamHI), and the construct expressed in insect cells. As above, the His-tagged E6-AP protein was purified by Ni^{+2} affinity, and the his-tag subsequently removed by treatment with enterokinase.

Alternatively, a HindIII (fill) to NotI fragment has been isolated from the pKS-E6AP construct and subsequently ligated into the SmaI - Not I sites of pGEX-4T-3, to produce a GST fusion protein in E. coli which was purified using a gluathione-sepharose resin.

v) Human p53

Human p53 (SEQ ID No. 18) was cloned into pBluescript II pKS+ from the HeLa cell cDNA library using the primers 5' $(GC)_3$GAATTCGCCATGGAGGAGCC-GCAGTCAGATCCT-3' and 5'-$(GC)_3$AAGCTT-TCAGTCTGAGTCAGGCCCTTCTGT-3'. In similar fashion to the other component proteins above, several different expression constructs were generated for p53, some of which included extra polypeptide sequence to facilitate purification. For expression in insect cells, two baculoviral constructs were made. For native p53, a BamHI fragment of the pKS-p53 vector was ligated into BamHI digested pVL1393. For His_6-tagged p53, the BamHI fragment was ligated into pBlueBacA previously cut with BamHI. Likewise, a GST-p53 was generated in E. coli by expression of a pGEX construct made by ligating a p53-containing EcoRI to NotI fragment of the pKS-p53 construct into pGEX-4T-1.

In the instance of each of the two fusion proteins, standard protocols were used to purify p53 from lysed transformants. For the native p53 produced by the pVL1393-p53 construct, the method of Hupp et al. was used to purify the p53 on a heparin-sepharose column (Hupp et al. (192) *Cell* 71:875-886).

vi) Ubiquitin

Ubiquitin is available from commercial sources (Bovine ubiquitin, Sigma catalog no. 6253; yeast ubiquitin, Sigma catalog no. 2129). Various modified forms of ubiquitin are also available as for example, fluorescein-labeled ubiquitin (Sigma catalog no. U5504), and horseradish-peroxidase labeled ubiquitin (Sigma catalog no. U9879). Biotinylated ubiquitin can be prepared from biotin-NHS (N-hydroxy-succinimide ester) using well-known techniques (biotinylation kit; Pierce catalog no. 214206, 203188 (6 atom spacer), or 203114 (14 atom spacer)).

vii) Additional Reagents

For generating certain of the detection means as described herein, some of the following reagents can be employed: polyclonal sera to ubiquitin (Sigma catalog no.

U5379); labeled antibodies to biotin (Sigma catalog nos. A4541 (peroxidase conjugated) and F6762 (FITC conjugated)); labeled avidin (Sigma catalog nos. A7294, E2636 (peroxidase conjugated) and A2050, E2761 (FITC conjugated)); streptavidin (Sigma catalog no. S3762 (FITC conjugated) and S5512 (peroxidase conjugated)); Streptavidin-coated beads (Sigma catalog no. 400996; Pierce catalog no. 20347G); Streptavidin-coated 96 well microtrite plates (Pierce catalog no. 15124); Maleic anhydride-activated polystyrene 96 well plates (Pierce catalog no. 15110); and antibody to human p53 (PharMingen catalog Nos. 14091A and 14211A).

Example 3

In vitro ubiquitination of p53

We describe the cloning of a new human ubiquitin-conjugating enzyme hUbCE in Example 1. In Examples 4 and 5, we show that hUbCE specifically ubiquitinylates E6AP and is involved in the turnover of p53 *in vivo*. We have defined several discrete biochemical steps in the activation and transfer of ubiquitin onto p53. These biochemical reactions provide two levels of specificity in the ubiquitination of p53; the hUbCE dependent ubiquitination of E6AP, and the E6-dependent transfer of ubiquitin from ubiquitinylated E6AP to p53.

Proteins. To perform an *in vitro* ubiquitination reaction, native hUbCE and UBC2, the human homolog of the *S.cerevisiae* DNA repair gene, Rad6 (Koken et al. (1991) *PNAS* 88:8865-8869) were expressed and purified from E.coli BL21(DE3). Both proteins are readily soluble and easily purified using standard procedures. The cloning and purification of each of the proteins hUbCE, UBC2, p53, human E1, E6, and E6AP are described in Example 2 above. Briefly, native p53 was expressed from the baculoviral vector pVL1392 in Sf9 insect cells according to the manufacturer's instructions (Pharmingen) and purified on a p53 affinity column. HPV18 E6 was expressed *E.coli* BL21 as a GST fusion protein and purified on GSH-sepharose. Human E1 was cloned by PCR from the published cDNA sequence (Handley et al. (1991) *PNAS* 88:258-262), and native protein was expressed and purified from baculoviral infected cells. E6AP was expressed in E.coli JM109 as a GST fusion protein and purified on GSH-sepharose.

Ubiquitination reactions. Ubiquitination reactions contained 50-200ng of the indicated proteins in 50mM Tris pH 7.5, 5mM $MgCl_2$, 2mM ATP-γ-S, 0.1 mM DTT and 5μM ubiquitin. Total reactions (30μl) were incubated at 25°C for 3hrs and then loaded on an 8% SDS gel for analysis of p53 ubiquitination or a 4-20% gradient gel for analysis of ubiquitination of the ubiquitin-conjugating enzymes and E6AP. The gels were run and proteins were electrophoretically transferred to nitrocellulose. p53 proteins were revealed with the monoclonal antibody DO-1 (Oncogene Science) and the ECL system from NEN. Ubiquitinylated proteins were visualized using Extravidin-HRP from Sigma and the ECL system from NEN.

As demonstrated in Figure 6, the appearance of specific p53-ubiquitin conjugates requires hUbCE, HPV18-E6, E6AP, ubiquitin and E1, the ubiquitin activating enzyme. In contrast, UBC2 was active in a minimal conjugation reaction containing E1, ATP and ubiquitin, in that E1 could activate ubiquitin and transfer it onto UBC2. However, UBC2 could not substitute for hUbCE in the p53 conjugation reaction (Fig. 2, lane 3). In addition, we made an active site cysteine-to-serine mutation in hUbCE. Such active site E2 mutants should accept activated ubiquitin from E1 but should not ubiquitinylate their downstream substrates owing to the high stability of the esther linkage formed between the active site serine and the carboxy-terminus of ubiquitin. This mutant was inactive in the p53 conjugation reaction (Fig. 6, lane 7). These results demonstrate that a catalytically active hUbCE is absolutely required for generation of ubiquitinylated p53 in this *in vitro* system.

In Figure 7A we show that ubiquitinated E1 could transfer ubiquitin efficiently to hUbCE but not directly to E6AP and that ubiquitinated hUbCE transferred ubiquitin to E6AP in a reaction that was not further stimulated by E6. All of these ubiquitination reactions required the presence of the ubiquitin-activating enzyme, E1, and ubiquitin.

To address the issue of the specificity of hUbCE-mediated ubiquitination of E6AP we performed ubiquitination reactions with purified recombinant hUbCE, GST-UBC2, GST-UBC8 (Kaiser et al. (1994) *J. Biol. Chem.* 269:8797-8802) and a GST-fusion of the so-called epidermal ubiquitin conjugating enzyme (Liu et al. (1992) *J Biol Chem* 267:15829-15835). Each of these recombinant proteins could accept activated ubiquitin from E1, but only hUbCE could donate ubiquitin to E6AP (Figure 7B). We also confirmed that native UBC2 could accept ubiquitin from E1 but could not donate ubiquitin to E6AP (data not shown).

We then purified the ubiquitinated E6AP by affinity chromatography on glutathione-Sepharose and demonstrated that it did not contain appreciable amounts of ubiquitinated E1, ubiquitinylated hUbCE or free ubiquitin. We found that this purified, ubiquitinated E6AP could donate ubiquitin to p53 in an E6-dependent reaction.

Example 4

Radiolabel-detection assay

^{35}S-labeled p53, prepared by cell culture technique utilizing ^{35}S-methionine, is incubated with combined purified components of a ubiquitin conjugating system, including biotinylated ubiquitin. The reaction is conducted in a 96 well microtitre plate and stopped with iodoacetate. The reaction mixture is transferred to the wells of a streptavidin-coated microtitre plate and incubated to capture the complex of biotinylated ubiquitin and p53 (free biotinylated ubiquitin will also compete for binding sites on the well). The wells are washed with buffer (e.g. phosphate-buffered saline, or conjugation buffer lacking ubiquitin and ATP) to remove uncomplexed p53. Ubiquinated p53 is detected by addition of scintillant to the

well and counting in a scintillation instrument. Inhibition of the ubiquitin conjugation system by an added candidate agent is indicated by a reduced radioactive count

Example 5

Immunodetection assay

p53 is incubated with combined purified components of a ubiquitin conjugating system as desribed above, including biotinylated ubiquitin. The reaction is conducted in a 96 well microtitre plate and stopped with iodoacetate. The reaction mixture is transferred to the wells of a streptavidin coated microtitre plate and incubated to capture the complex of biotinylated ubiquitin and p53 (free biotinylated ubiquitin will also compete for binding sites on the well). The wells are washed with buffer to remove uncomplexed p53. Next, the ub:p53 complexes capatured on the plate are decorated with a murine monoclonal antibody to p53. The wells are washed and binding of monoclonal antibody is detected by addition of peroxidase-conjugated antibody to mouse IgG (H+L) (Pierce catalog nos. 91430G and 91450G) and contacting with an appropriate substrate system, such as o-phenylenediamine dihydrochloride (Sigma catalog no. P9187).

Example 6

GST detection assay

The GST-p53 fusion product is incubated with combined purified components of a ubiquitin conjugating system, including biotinylated ubiquitin. The reaction is conducted in a 96 well microtitre plate and stopped with iodoacetate. The reaction mixture is transferred to the wells of a streptavidin coated microtitre plate and incubated to capture the complex of biotinylated ubiquitin and GST-p53 (free biotinylated ubiquitin will also compete for binding sites on the well). The wells are washed with buffer to remove uncomplexed GST-p53 . Binding of ubiquitinated GST-p53 is monitored with a detection system, based either on a biochemical assay for GST (e.g., 1-chloro-2,4-dinitrobenzene, Pharmacia catalog no. 27-4590-01) or an immunological assay using goat anti-GST antibody (Pharmacia catalog no. 27-4590-01).

Example 7

Reporter construct detection assay

The plasmid pTK*luc*, shown in Figure 9, comprises a luciferase gene whose expression is driven by the core Herpes simplex virus thymidine-kinase (TK) promoter which has been modified with either p53 (p53RE/TK), myc (mycRE/TK), or Sp1 (Sp1RE/TK) binding sites. When the construct lacking any of the modifications to the TK promoter is transfected into mammalian cells, the detectable luciferase activity is low because this core TK promoter fragment does not contain the upstream activating sequences necessary for

efficient transcriptional activation of the luciferase gene. However transfection with the constructs in which TK is further modified to contain either 3 or 6 response-elements (RE) for one of p53, myc or Sp1, the detectable luciferase activity increases in cells which express the appropriate protein. For example, the level of luciferase expression is significantly higher in p53-producing cells (e.g. ML1 cells) transfected with the p53RETK- containing construct than with the TK construct. Likewise, endogenous myc and Sp1 proteins can drive expression of the mycRE/TK and Sp1RE/TK constructs. As set out above, both p53 and myc can be degraded by the ubiquitin pathway. However, Sp1 is not known to be degraded by any ubiquitin-mediated pathway, and the SP1RE/TK construct can therefore be used as a control in the present assays. Thus, in the presence of an agent which inhibits ubiquitin-mediated degradation of p53 in a cell harboring the p53RE/TK construct, the level of luciferase activity would increase relative to that in the cell not treated with the candidate agent.

To construct the luciferase reporter constructs shown in Figure 9, the pGL2-Basic vector (Promega catalog no. E1641) was modified by addition, in the multiple cloning region, of a SalI to BamHI fragment containing the TK promoter sequence with either 3 or 6 tandemly arranged binding sites placed upstream of the TK promoter. Prior to addition of the RE/TK promoter sequences, a SalI restriction site at 2744 of pGL2-Basic was destroyed by oligonucleotide site-directed mutagenesis. The resulting constructs, designated p53RE/TK, mycRE/TK, and Sp1RE/TK, were each subsequently used to transfect mammalian cells following the manufacturer's suggests (Technical notes, Part #TM003 of Promega Catalog no. E164).

In an alternative embodiment, a Sal1 to BamH1 fragment of p53/RE/TK containing the luciferase reporter gene was isolated and sub-cloned into another eukaryotic expression vector pcDNAIII (Invitrogen, San Diego, CA) previously digested with BglII and XhoI.

The vector p53RE/TK is transfected into the human chronic leukemia cell line MLI that expresses wild-type p53. In this *in vivo* situation, luciferase expression is upregulated by the presence of p53, which functions as a transcriptional activating factor by binding to the p53 response element upstream of the TK promoter. The ubiquitin conjugating system participates in the degradation of p53 and, when functional, down regulates the expression of luciferase in this system. Measurement of luciferase activity are carried out by standard protocols (see, for example, Promega Technical Bulletin #TB161). Cells are grown and transfected in a tissue culture grade 96 well microtitre plate. The cultured cells are incubated in the presence and absence of a candidate agent, then harvested and centrifuged. The harvested cells are then lysed with lysis buffer. The lysates clarified by centrifugation, and the supernatants transferred to luminescent grade microtitre plates. Luciferase assay sustrate (Beetle luciferin, Promega catalog no. E1603) is added, and the reaction in each well monitored in a luminometer or scintillation counter. Inhibition of the ubiquitin conjugating

system results in a greater luminescence signal than the uninhibited system. Although an *in vivo* assay, this screen will ignore general cytotoxic compounds .

Example 8

Microinjection of Sense and Anti-sense constructs of the hUbCE Gene

To investige the consequences of interfering with hUbCE and E6AP function in p53 degradation, we performed microinjection experiments using sense and anti-sense constructs of the hUbCE gene. To facilitate the detection of p53 by indirect immunofluorescence, the experiments were performed in the human tumor cell line MDA-MB-468 which contain high levels of mutant p53 (Arg273His). In this line, the degradation of p53 could be stimulated by microinjection of an HPV-18 E6 expression plasmid.

In order to determine whether hUbCE and E6AP mediate the E6-dependent ubiquitination and degradation of p53 *in vivo* co-injection experiments were performed. To briefly describe the experiments, the CMV expression vectors were obtained by inserting the entire open-reading frame of one of HPV-18 E6, human E1, human E6-AP, hUbCE, or a Cys-85 mutant of hUbCE, in either a sense or anti-sense orientation (as indicated in Figure 8) in the pX-plasmid (Baldin et al. (1993) *Genes & Devel.*, 7:812-821). Plasmids were purified with a Promega Wizard Maxi-prep kit and injected at a concentration of 50 to 100 μg/μl in the presence of normal affinity-purified rabbit or mouse antibody (5 mg/ml in PBS) used as microinjection marker.

Cell monolayers of asynchronous MDA-MB-468 cells were injected with the indicated DNAs (Figure 8) along with rabbit IgG to allow identification of injected cells with an automated microinjection system (AIS, Zeiss; Ansorge et al. (1988) *J. Biochem. Biophys. Meth.*, 16:283-292). All microinjection experiments were carried out in 3.5 cm Petri dishes containing 3 ml of DMEM medium carbonate free, in order to avoid the decrease in pH of the medium during the injection. Each cell was injected at a pressure between 50 and 150 hPa. After 24hrs the cells were fixed and stained with a p53 specific monoclonal antibody (DO-1; Oncogene Sciences) followed by a biotinylated horse anti-rabbit antibody and Texas red conjugated streptavidin. Injected cells were identified by staining with an FITC conjugated goat anti-rabbit antibody (Baldin et al. (1993) *Genes and Dev* 7:812-821).

When either an anti-sense or mutant hUbCE expression plasmid or an expression plasmid encoding anti-sense E6AP was co-injected with the E6 expression plasmid, the E6 stimulated degradation of p53 was inhibited (Figure 8). Similar results were obtained when polyclonal antibodies generated against human hUbCE or an expression plasmid encoding a mutant form of E6AP were microinjected (not shown).

Co-injection of an E6 expression plasmid with an expression plasmid encoding anti-sense E1 also inhibited the E6 stimulated degradation of p53. Co-injection of anti-sense or mutant UBC2 expression plasmids had a negligible effect on the E6 stimulated degradation of p53 (Figure 8).

Moreover, the data that an hUbCE mutant, Cys-85→Ser, which produces an inactive form of the enzyme, is possibly a dominant negative mutant able to at least partially rescue p53.

Example 9

Generating a Molecular Model of the hUbCE protein

The three dimenstional coordinates of the protein backbone from the structure of UBC1 from *A. thaliana* (Brookhaven databank file 1AAK.pdb) were used for homology modeling of hUbCE. Modeling was performed with the Protein Workbench software package of QUANTA, version 4 (MSI, Burlington MA).

Briefly, the amino acid sequence of hUbCE (SEQ ID No. 2) and UBC1 were aligned using the alignment program in QUANTA. This alignment shows a 44% match of similar residues. The coordinates of the backbone non-hydrogen atoms were then copied onto the hUbCE sequence, sidechain coordinates for the hUbCE model were a ignored at this point. The resulting hUbCE structure was then energy minimized using 200 steps of the steepest descent algorithm followed by 5000 steps of the adopted-base Newton Raphson algorithm. All atoms, including polar hydrogens and all side chains were allowed to move. The resulting CHARMM energy of the system was -7084.2 kcal.

In the next step, the structure was heated up to 500°K using 2000 steps or a total time of 2 psec. After heating, the system was then allowed to equilibrate for 9 psec (9000 steps). The final CHARMM energy after 10 psec was around -5750 kcal. Finally, the system was cooled down to 300°K in steps of 50°K (1psec cooling, 4 psec equilibration) and finally equilibrated at 300°K for 6 psec. The final total CHARMM energy was around -6650 kcal. The final structure hsowed no serious conformational strains or improper angles. The atomic coordinates for the full length model are shown in Figure 1.

In the next step we modeled the 4-meric peptide Ala-Ile-Arg-Gly into the active site. This peptide was derived from the c-terminal sequence of ubiquitin (RIRG). A thioester bond was manually constructed in both cases between the C-terminal Gly and the active site cyteseines. The system was energy-minimized and subsequently subjected to molecular dynamics simulations. In both cases the Ile residue of the peptide settles into the hydrophobic pocket. There are two backbone-backbone hydrogen bonds between the loops and the peptide. The Arg of the peptide forms hydrogen bonds with a conserved Asp residue (between the conserved Val and Ile residues) in both cases.

The general tight fit of the peptide into the active-site cleft makes us very confident that this area is also the docking site for ubiquitin. We will use this structural information for the construction of various mutants which we believe will no longer bind ubiquitin. We will also use this three-dimensional information for the design of inhibitory peptides or peptidomimetics. The coordinates for the subset of residues determined to be of greatest import in rational drug design are shown in Figure 2.

Example 10

Cloning of Yeast UbCE Genes

In order to clone homologs of the hUbCE gene, degenerate oligonucleotides based on the conserved regions PVGDDLFHWH/Q and ITLAPSW (see SEQ ID No. 1) were designed and used to amplify *S. pombe* genomic DNA and cDNA in λZAP (strain h+^{N}his3-) and *C. albicans genomic* and cDNA in λZAP (strain 3153A). The amplification consisted of 30 cycles of 94°C for 1 minute, 55°C for 1 minute and 72°C for 1 minute. The PCR reactions were separated on a 2.5% low melting agarose gel, that identified a 250 bp fragment for both genomic and complementary DNA from *C. albicans*. From *S. pombe* 250 and 650 bp fragments were detected for complementary and genomic DNA respectively. The size discrepancy between complementary DNA and genomic *S. pombe* DNA fragments probably reflects the presence of an intron. The fragments of 250 bps were eluted and cloned into pCRII (TA cloning system, Invitrogen corporation).

The *S. pombe* and *C. albicans* DNA probes were ^{32}P labeled by nick translation and used on Southern blots to confirm the species identity of the fragments and to screen *S. pombe* and *C. albicans* cDNA libraries. Sequencing of the full length cDNAs confirmed the identity of the clones. The *C. albicans* and *S. pombe UbCE* open-reading frames are both 147 aa residues long (SEQ ID Nos: 3 and 5, respectively). The newly isolated genes are named caUbCE and spUbCE for *C. albicans* and *S. pombe* respectively.

Example 11

Cloning of the Human rapUBC Enzyme

Utilizing a two hybrid assay comprising an FKBP12-bait protein, a drug-dependent interaction trap assay was used to screen a WI38 (mixed G_0 and dividing fibroblast) cDNA library (Clonetech, Palo Alto CA) in pGADGH (XhoI insert, Clonetech). Briefly, the two hybrid assay was carried out in an HF7C yeast cell (Clonetech) in which FKB1 gene was disrupted. Of the clones isolated, a novel human ubiquitin-conjugating enzyme (rap-UBC, SEQ ID Nos. 12 and 13) has been identified. The original clones contained 5' end of the gene which included substantial portion of the coding region for rapUBC, including the active site cysteine and the 3' end of the gene. In order to obtain full length sequence of the rapUBC gene, the 5' end was cloned using a library vector (MTXP37) and oligos corresponding to sequences near the 5' end of the original cDNA clone SMR4-15. The oligos used were: VB1040: CTACTAATAGGTAGAAGCGGTGG (SEQ ID No:20) and VB1041: GGTAAA-CCAAAGCCCGACAGGG (SEQ ID No:21). PCR products were obtained from a cDNA library made from normal human fibroblasts (dividing WI38 cells).

Example 12

Ubiquitination of p27 by UBC3

We have found that human CDC34 (UBC3) is able to charge p27 (also called lck, Kip1 and Pic2) in a thioester and ubquitination assay. Briefly, ubiquitination reactions were performed as described above. Each reaction contained 50-200ng of the E1, E2 and p27 proteins in 50mM Tris pH 7.5, 5mM $MgCl_2$, 2mM ATP-γ-S, 0.1 mM DTT and 5μM ubiquitin. Total reactions (30μl) were incubated at 25°C for 3hrs and then loaded on an 12.5% SDS gel for analysis of p27 ubiquitination. The gel was run and proteins were electrophoretically transferred to nitrocellulose. p27 proteins were revealed with a commercially available monoclonal antibody (Transduction Laboratory) and the ECL system from NEN. Ubiquitinylated proteins were visualized using Extravidin-HRP from Sigma and the ECL system from NEN.

All of the above-cited references and publications are hereby incorporated by reference.

Equivalents

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
(A) NAME: Mitotix, Inc.
(B) STREET: One Kendall Square, Building 600
(C) CITY: Cambridge
(D) STATE: MA
(E) COUNTRY: USA
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(G) TELEPHONE: (617) 225-0001
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(ii) TITLE OF INVENTION: Ubiquitin Conjugating Enzymes

(iii) NUMBER OF SEQUENCES: 21

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII (text)

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/176,934
(B) FILING DATE: 04-JAN-1994

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/247,904
(B) FILING DATE: 23-MAY-1994

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/250,795
(B) FILING DATE: 27-MAY-1994

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/305,520
(B) FILING DATE: 13-SEP-1994

(2) INFORMATION FOR SEQ ID No:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 444 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..441

(xi) SEQUENCE DESCRIPTION: SEQ ID No:1:

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Met Ala Leu Lys Arg Ile His Lys Glu Leu Asn Asp Leu Ala Arg Asp
  1               5                  10                  15

CCT CCA GCA CAG TGT TCA GCA GGT CCT GTT GGA GAT GAT ATG TTC CAT        96
Pro Pro Ala Gln Cys Ser Ala Gly Pro Val Gly Asp Asp Met Phe His
            20                  25                  30

TGG CAA GCT ACA ATA ATG GGG CCA AAT GAC AGT CCC TAT CAG GGT GGA       144
Trp Gln Ala Thr Ile Met Gly Pro Asn Asp Ser Pro Tyr Gln Gly Gly
        35                  40                  45

GTA TTT TTC TTG ACA ATT CAT TTC CCA ACA GAT TAC CCC TTC AAA CCA       192
Val Phe Phe Leu Thr Ile His Phe Pro Thr Asp Tyr Pro Phe Lys Pro
    50                  55                  60

CCT AAG GTT GCA TTT ACC ACA AGA ATT TAT CAT CCA AAT ATT AAC AGT       240
Pro Lys Val Ala Phe Thr Thr Arg Ile Tyr His Pro Asn Ile Asn Ser
65                  70                  75                  80

AAT GGC AGC ATT TGT CTT GAT ATT CTA CGA TCA CAG TGG TCT CCA GCA       288
Asn Gly Ser Ile Cys Leu Asp Ile Leu Arg Ser Gln Trp Ser Pro Ala
                85                  90                  95

CTA ACT ATT TCA AAA GTA CTC TTG TCC ATC TGT TCT CTG TTG TGT GAT       336
Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Cys Asp
            100                 105                 110

CCC AAT CCA GAT GAT CCT TTA GTG CCT GAG ATT GCT CGG ATC TAC CAA       384
Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala Arg Ile Tyr Gln
        115                 120                 125

ACA GAT AGA GAA AAG TAC AAC AGA ATA GCT CGG GAA TGG ACT CAG AAG       432
Thr Asp Arg Glu Lys Tyr Asn Arg Ile Ala Arg Glu Trp Thr Gln Lys
    130                 135                 140

TAT GCG ATG TAA                                                      444
Tyr Ala Met
145
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(2) INFORMATION FOR SEQ ID No:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID No:2:

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Pro Pro Ala Gln Cys Ser Ala Gly Pro Val Gly Asp Asp Met Phe His
            20                  25                  30
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Trp Gln Ala Thr Ile Met Gly Pro Asn Asp Ser Pro Tyr Gln Gly Gly
          35                  40                  45

Val Phe Phe Leu Thr Ile His Phe Pro Thr Asp Tyr Pro Phe Lys Pro
      50                  55                  60

Pro Lys Val Ala Phe Thr Thr Arg Ile Tyr His Pro Asn Ile Asn Ser
 65                  70                  75                  80

Asn Gly Ser Ile Cys Leu Asp Ile Leu Arg Ser Gln Trp Ser Pro Ala
                 85                  90                  95

Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Cys Asp
            100                 105                 110

Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala Arg Ile Tyr Gln
        115                 120                 125

Thr Asp Arg Glu Lys Tyr Asn Arg Ile Ala Arg Glu Trp Thr Gln Lys
    130                 135                 140

Tyr Ala Met
145
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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 582 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 25..465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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CACGAGTAAC TATTGCTTTA AATC ATG TCA TTA AAA CGT ATT AAC AAA GAA      51
                           Met Ser Leu Lys Arg Ile Asn Lys Glu
                             1               5

TTA TCT GAC TTA GGA AGA GAT CCA CCA TCA TCA TGT TCA GCC GGT CCA      99
Leu Ser Asp Leu Gly Arg Asp Pro Pro Ser Ser Cys Ser Ala Gly Pro
 10                  15                  20                  25

GTT GGA GAT GAC TTA TAC CAC TGG CAA GCA TCT ATC ATG GGA CCA CCA     147
Val Gly Asp Asp Leu Tyr His Trp Gln Ala Ser Ile Met Gly Pro Pro
                 30                  35                  40

GAC TCT CCA TAC GCT GGT GGG GTA TTT TTC TTG AGT ATC CAT TTC CCA     195
Asp Ser Pro Tyr Ala Gly Gly Val Phe Phe Leu Ser Ile His Phe Pro
             45                  50                  55
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ACA GAT TAT CCT TTA AAA CCA CCA AAG ATT GCT TTA ACA ACA AAA ATC       243
Thr Asp Tyr Pro Leu Lys Pro Pro Lys Ile Ala Leu Thr Thr Lys Ile
          60                  65                  70

TAT CAT CCA AAT ATT AAT AGT AAT GGT AAC ATC TGT TTA GAT ATC TTA       291
Tyr His Pro Asn Ile Asn Ser Asn Gly Asn Ile Cys Leu Asp Ile Leu
     75                  80                  85

AAG GAT CAA TGG TCA CCT GCA TTA ACA ATT TCC AAA GTG TTA TTG TCT       339
Lys Asp Gln Trp Ser Pro Ala Leu Thr Ile Ser Lys Val Leu Leu Ser
 90                  95                 100                 105

ATT TGT TCA TTA TTA ACT GAT GCC AAC CCA GAC GAT CCA TTA GTG CCA       387
Ile Cys Ser Leu Leu Thr Asp Ala Asn Pro Asp Asp Pro Leu Val Pro
                110                 115                 120

GAA ATC GCT CAC ATT TAT AAA CAA GAT AGA AAG AAG TAT GAA GCT ACT       435
Glu Ile Ala His Ile Tyr Lys Gln Asp Arg Lys Lys Tyr Glu Ala Thr
            125                 130                 135

GCC AAA GAA TGG ACT AAG AAA TAT GCT GTG TGATTTTAGA GAAAAACAAA        485
Ala Lys Glu Trp Thr Lys Lys Tyr Ala Val
        140                 145

AACATCTAAT TTCTACATGT ATTATGTCGT AATGCTTTCA CACAATACAA AAACATCTAA     545

TTTCTACATG TATTATGTCG TAATGCTTTC ACACAAT                              582
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Ser Leu Lys Arg Ile Asn Lys Glu Leu Ser Asp Leu Gly Arg Asp
  1               5                  10                  15

Pro Pro Ser Ser Cys Ser Ala Gly Pro Val Gly Asp Asp Leu Tyr His
             20                  25                  30

Trp Gln Ala Ser Ile Met Gly Pro Pro Asp Ser Pro Tyr Ala Gly Gly
         35                  40                  45
```

```
Val Phe Phe Leu Ser Ile His Phe Pro Thr Asp Tyr Pro Leu Lys Pro
     50                  55                  60

Pro Lys Ile Ala Leu Thr Thr Lys Ile Tyr His Pro Asn Ile Asn Ser
 65                  70                  75                  80

Asn Gly Asn Ile Cys Leu Asp Ile Leu Lys Asp Gln Trp Ser Pro Ala
                 85                  90                  95

Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp
            100                 105                 110

Ala Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His Ile Tyr Lys
        115                 120                 125

Gln Asp Arg Lys Lys Tyr Glu Ala Thr Ala Lys Glu Trp Thr Lys Lys
    130                 135                 140

Tyr Ala Val
145
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 522 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 22..462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
CGCAAAAGCA AACCAGTAAC G ATG GCT TTG AAA AGA ATT AAC CGT GAA TTA        51
                        Met Ala Leu Lys Arg Ile Asn Arg Glu Leu
                          1               5                  10

GCT GAT CTT GGA AAA GAC CCA CCG TCT TCT TGT TCC GCC GGC CCT GTT        99
Ala Asp Leu Gly Lys Asp Pro Pro Ser Ser Cys Ser Ala Gly Pro Val
                 15                  20                  25

GGC GAT GAT TTA TTC CAT TGG CAA GCT ACA ATC ATG GGT CCT GCT GAC       147
Gly Asp Asp Leu Phe His Trp Gln Ala Thr Ile Met Gly Pro Ala Asp
             30                  35                  40

AGC CCT TAT GCG GGT GGT GTC TTC TTC TTG TCC ATT CAT TTC CCT ACG       195
Ser Pro Tyr Ala Gly Gly Val Phe Phe Leu Ser Ile His Phe Pro Thr
         45                  50                  55
```

```
GAC TAC CCA TTC AAG CCA CCA AAG GTA AAC TTT ACA ACC AGA ATC TAT       243
Asp Tyr Pro Phe Lys Pro Pro Lys Val Asn Phe Thr Thr Arg Ile Tyr
     60                  65                  70

CAT CCC AAC ATC AAT TCA AAC GGT AGC ATT TGT TTG GAT ATC CTT CGT       291
His Pro Asn Ile Asn Ser Asn Gly Ser Ile Cys Leu Asp Ile Leu Arg
 75                  80                  85                  90

GAC CAA TGG TCT CCA GCG TTG ACT ATA TCA AAG GTA TTA CTG TCT ATC       339
Asp Gln Trp Ser Pro Ala Leu Thr Ile Ser Lys Val Leu Leu Ser Ile
                 95                 100                 105

TGC TCA TTG TTG ACA GAT CCT AAT CCT GAT GAT CCG CTT GTG CCT GAA       387
Cys Ser Leu Leu Thr Asp Pro Asn Pro Asp Asp Pro Leu Val Pro Glu
            110                 115                 120

ATT GCG CAC GTC TAC AAA ACT GAC AGA TCC CGT TAT GAA TTA AGT GCT       435
Ile Ala His Val Tyr Lys Thr Asp Arg Ser Arg Tyr Glu Leu Ser Ala
        125                 130                 135

CGT GAA TGG ACT AGA AAA TAC GCA ATC TAGAGTTTGT TTCTGTGTTG             482
Arg Glu Trp Thr Arg Lys Tyr Ala Ile
    140                 145

ATATTAAATA TTCATCTCTT AAAAAAAAAA AAAAAACTCG                           522
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Met Ala Leu Lys Arg Ile Asn Arg Glu Leu Ala Asp Leu Gly Lys Asp
 1               5                  10                  15

Pro Pro Ser Ser Cys Ser Ala Gly Pro Val Gly Asp Asp Leu Phe His
            20                  25                  30

Trp Gln Ala Thr Ile Met Gly Pro Ala Asp Ser Pro Tyr Ala Gly Gly
        35                  40                  45

Val Phe Phe Leu Ser Ile His Phe Pro Thr Asp Tyr Pro Phe Lys Pro
    50                  55                  60

Pro Lys Val Asn Phe Thr Thr Arg Ile Tyr His Pro Asn Ile Asn Ser
65                  70                  75                  80

Asn Gly Ser Ile Cys Leu Asp Ile Leu Arg Asp Gln Trp Ser Pro Ala
                85                  90                  95
```

Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp
100 105 110

Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His Val Tyr Lys
115 120 125

Thr Asp Arg Ser Arg Tyr Glu Leu Ser Ala Arg Glu Trp Thr Arg Lys
130 135 140

Tyr Ala Ile
145

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Xaa Leu Lys Arg Ile Xaa Xaa Glu Leu Xaa Asp Leu Xaa Xaa Asp
1 5 10 15

Pro Pro Xaa Xaa Cys Ser Ala Gly Pro Val Gly Asp Asp Xaa Xaa His
20 25 30

Trp Gln Ala Xaa Ile Met Gly Pro Asn Asp Ser Pro Tyr Xaa Gly Gly
35 40 45

Val Phe Phe Leu Xaa Ile His Phe Pro Thr Asp Tyr Pro Xaa Lys Pro
50 55 60

Pro Lys Xaa Xaa Xaa Thr Thr Xaa Ile Tyr His Pro Asn Ile Asn Ser
65 70 75 80

Asn Gly Xaa Ile Cys Leu Asp Ile Leu Xaa Xaa Gln Trp Ser Pro Ala
85 90 95

Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Xaa Asp
100 105 110

Xaa Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala Xaa Xaa Tyr Xaa
115 120 125

Xaa Asp Arg Xaa Xaa Tyr Xaa Xaa Xaa Ala Xaa Glu Trp Thr Xaa Lys
130 135 140

Tyr Ala Xaa
145

(2) INFORMATION FOR SEQ ID No:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID No:8:

GCGCGCAAGC TTTAYGARGG WGGWGTYTTY TT 32

(2) INFORMATION FOR SEQ ID No:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID No:9:

GCGCGCGAAT TCACNGCRTA YTTYTTNGTC CCAYTC 36

(2) INFORMATION FOR SEQ ID No:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID No:10:

GCGCGCAAGC TTCCNGTNGG NGAYTTRTTY CAYTGGCA 38

(2) INFORMATION FOR SEQ ID No:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID No:11:

GCGCGCGAAT TCATNGTNAR NGCNGGCGAC CA 32

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 907 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 34..507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
GCCGGGGCTG CGGCCGCCCG AGGGACTTTG AAC ATG TCG GGG ATC GCC CTC AGC        54
                                      Met Ser Gly Ile Ala Leu Ser
                                        1               5

AGA CTC GCC CAG GAG AGG AAA GCA TGG AGG AAA GAC CAC CCA TTT GGT       102
Arg Leu Ala Gln Glu Arg Lys Ala Trp Arg Lys Asp His Pro Phe Gly
         10                  15                  20

TTC GTG GCT GTC CCA ACA AAA AAT CCC GAT GGC ACG ATG AAC CTC ATG       150
Phe Val Ala Val Pro Thr Lys Asn Pro Asp Gly Thr Met Asn Leu Met
     25                  30                  35

AAC TGG GAG TGC GCC ATT CCA GGA AAG AAA GGG ACT CCG TGG GAA GGA       198
Asn Trp Glu Cys Ala Ile Pro Gly Lys Lys Gly Thr Pro Trp Glu Gly
 40                  45                  50                  55

GGC TTG TTT AAA CTA CGG ATG CTT TTC AAA GAT GAT TAT CCA TCT TCG       246
Gly Leu Phe Lys Leu Arg Met Leu Phe Lys Asp Asp Tyr Pro Ser Ser
                 60                  65                  70

CCA CCA AAA TGT AAA TTC GAA CCA CCA TTA TTT CAC CCG AAT GTG TAC       294
Pro Pro Lys Cys Lys Phe Glu Pro Pro Leu Phe His Pro Asn Val Tyr
             75                  80                  85

CCT TCG GGG ACA GTG TGC CTG TCC ATC TTA GAG GAG GAC AAG GAC TGG       342
Pro Ser Gly Thr Val Cys Leu Ser Ile Leu Glu Glu Asp Lys Asp Trp
         90                  95                  100

AGG CCA GCC ATC ACA ATC AAA CAG ATC CTA TTA GGA ATA CAG GAA CTT       390
Arg Pro Ala Ile Thr Ile Lys Gln Ile Leu Leu Gly Ile Gln Glu Leu
     105                 110                 115
```

```
CTA AAT GAA CCA AAT ATC CAA GAC CCA GCT CAA GCA GAG GCC TAC ACG      438
Leu Asn Glu Pro Asn Ile Gln Asp Pro Ala Gln Ala Glu Ala Tyr Thr
120                 125                 130                 135

ATT TAC TGC CAA AAC AGA GTG GAG TAC GAG AAA AGG GTC CGA GCA CAA      486
Ile Tyr Cys Gln Asn Arg Val Glu Tyr Glu Lys Arg Val Arg Ala Gln
                140                 145                 150

GCC AAG AAG TTT GCG CCC TCA TAAGCAGCGA CCTTGTGGCA TCGTCAAAAG          537
Ala Lys Lys Phe Ala Pro Ser
            155

GAAGGGATTG GTTTGGCAAG AACTTGTTTA CAACATTTTT GGCAAATCTA AAGTTGCTCC     597

ATACAATGAC TAGTCACCTG GGGGGGTTGG GCGGGCGCCA TCTTCCATTG CCGCCGCGGG     657

TGTGCGGTCT CGATTCGCTG AATTGCCCGT TTCCATACAG GGTCTCTTCC TTCGGTCTTT     717

TGGTATTTTT GGATTGTTAT GTAAAACTCG CTTTTATTTT AATATTGATG TCAGTATTTC     777

AACTGCTGTA AAATTATAAA CTTTTATACT GGGTAAGTCC CCCAGGGGCG AGTTNCCTCG     837

CTCTGGGATG CAGGCATGCT TCTCACCGTG CAGAGCTGCA CTTGNCCTCA GCTGNCTGNA     897

TGGAAATGCA                                                           907
```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
Met Ser Gly Ile Ala Leu Ser Arg Leu Ala Gln Glu Arg Lys Ala Trp
 1               5                  10                  15

Arg Lys Asp His Pro Phe Gly Phe Val Ala Val Pro Thr Lys Asn Pro
            20                  25                  30

Asp Gly Thr Met Asn Leu Met Asn Trp Glu Cys Ala Ile Pro Gly Lys
        35                  40                  45

Lys Gly Thr Pro Trp Glu Gly Gly Leu Phe Lys Leu Arg Met Leu Phe
    50                  55                  60

Lys Asp Asp Tyr Pro Ser Ser Pro Pro Lys Cys Lys Phe Glu Pro Pro
65                  70                  75                  80

Leu Phe His Pro Asn Val Tyr Pro Ser Gly Thr Val Cys Leu Ser Ile
                85                  90                  95
```

```
Leu Glu Glu Asp Lys Asp Trp Arg Pro Ala Ile Thr Ile Lys Gln Ile
            100                 105                 110

Leu Leu Gly Ile Gln Glu Leu Leu Asn Glu Pro Asn Ile Gln Asp Pro
        115                 120                 125

Ala Gln Ala Glu Ala Tyr Thr Ile Tyr Cys Gln Asn Arg Val Glu Tyr
    130                 135                 140

Glu Lys Arg Val Arg Ala Gln Ala Lys Lys Phe Ala Pro Ser
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..3177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
ATG TCC AGC TCG CCG CTG TCC AAG AAA CGT CGC GTG TCC GGG CCT GAT      48
Met Ser Ser Ser Pro Leu Ser Lys Lys Arg Arg Val Ser Gly Pro Asp
  1               5                  10                  15

CCA AAG CCG GGT TCT AAC TGC TCC CCT GCC CAG TCC GTG TTG TCC GAA      96
Pro Lys Pro Gly Ser Asn Cys Ser Pro Ala Gln Ser Val Leu Ser Glu
            20                  25                  30

GTG CCC TCG GTG CCA ACC AAC GGA ATG GCC AAG AAC GGC AGT GAA GCA     144
Val Pro Ser Val Pro Thr Asn Gly Met Ala Lys Asn Gly Ser Glu Ala
        35                  40                  45

GAC ATA GAC GAG GGC CTT TAC TCC CGG CAG CTG TAT GTG TTG GGC CAT     192
Asp Ile Asp Glu Gly Leu Tyr Ser Arg Gln Leu Tyr Val Leu Gly His
    50                  55                  60

GAG GCA ATG AAG CGG CTC CAG ACA TCC AGT GTC CTG GTA TCA GGC CTG     240
Glu Ala Met Lys Arg Leu Gln Thr Ser Ser Val Leu Val Ser Gly Leu
65                  70                  75                  80

CGG GGC CTG GGC GTG GAG ATC GCT AAG AAC ATC ATC CTT GGT GGG GTC     288
Arg Gly Leu Gly Val Glu Ile Ala Lys Asn Ile Ile Leu Gly Gly Val
                85                  90                  95

AAG GCT GTT ACC CTA CAT GAC CAG GGC ACT GCC CAG TGG GCT GAT CTT     336
Lys Ala Val Thr Leu His Asp Gln Gly Thr Ala Gln Trp Ala Asp Leu
            100                 105                 110
```

```
TCC TCC CAG TTC TAC CTG CGG GAG GAG GAC ATC GGT AAA AAC CGG GCC      384
Ser Ser Gln Phe Tyr Leu Arg Glu Glu Asp Ile Gly Lys Asn Arg Ala
        115                 120                 125

GAG GTA TCA CAG CCC CGC CTC GCT GAG CTC AAC AGC TAT GTG CCT GTC      432
Glu Val Ser Gln Pro Arg Leu Ala Glu Leu Asn Ser Tyr Val Pro Val
    130                 135                 140

ACT GCC TAC ACT GGA CCC CTC GTT GAG GAC TTC CTT AGT GGT TTC CAG      480
Thr Ala Tyr Thr Gly Pro Leu Val Glu Asp Phe Leu Ser Gly Phe Gln
145                 150                 155                 160

GTG GTG GTG CTC ACC AAC ACC CCC CTG GAG GAC CAG CTG CGA GTG GGT      528
Val Val Val Leu Thr Asn Thr Pro Leu Glu Asp Gln Leu Arg Val Gly
                165                 170                 175

GAG TTC TGT CAC AAC CGT GGC ATC AAG CTG GTG GTG GCA GAC ACG CGG      576
Glu Phe Cys His Asn Arg Gly Ile Lys Leu Val Val Ala Asp Thr Arg
            180                 185                 190

GGC CTG TTT GGG CAG CTC TTC TGT GAC TTT GGA GAG GAA ATG ATC CTC      624
Gly Leu Phe Gly Gln Leu Phe Cys Asp Phe Gly Glu Glu Met Ile Leu
        195                 200                 205

ACA GAT TCC AAT GGG GAG CAG CCA CTC AGT GCT ATG GTT TCT ATG GTT      672
Thr Asp Ser Asn Gly Glu Gln Pro Leu Ser Ala Met Val Ser Met Val
    210                 215                 220

ACC AAG GAC AAC CCC GGT GTG GTT ACC TGC CTG GAT GAG GCC CGA CAC      720
Thr Lys Asp Asn Pro Gly Val Val Thr Cys Leu Asp Glu Ala Arg His
225                 230                 235                 240

GGG TTT GAG AGC GGG GAC TTT GTC TCC TTT TCA GAA GTA CAG GGC ATG      768
Gly Phe Glu Ser Gly Asp Phe Val Ser Phe Ser Glu Val Gln Gly Met
                245                 250                 255

GTT GAA CTC AAC GGA AAT CAG CCC ATG GAG ATC AAA GTC CTG GGT CCT      816
Val Glu Leu Asn Gly Asn Gln Pro Met Glu Ile Lys Val Leu Gly Pro
            260                 265                 270

TAT ACC TTT AGC ATC TGT GAC ACC TCC AAC TTC TCC GAC TAC ATC CGT      864
Tyr Thr Phe Ser Ile Cys Asp Thr Ser Asn Phe Ser Asp Tyr Ile Arg
        275                 280                 285

GGA GGC ATC GTC AGT CAG GTC AAA GTA CCT AAG AAG ATT AGC TTT AAA      912
Gly Gly Ile Val Ser Gln Val Lys Val Pro Lys Lys Ile Ser Phe Lys
    290                 295                 300

TCC TTG GTG GCC TCA CTG GCA GAA CCT GAC TTT GTG GTG ACG GAC TTC      960
Ser Leu Val Ala Ser Leu Ala Glu Pro Asp Phe Val Val Thr Asp Phe
305                 310                 315                 320

GCC AAG TTT TCT CGC CCT GCC CAG CTG CAC ATT GGC TTC CAG GCC CTG     1008
Ala Lys Phe Ser Arg Pro Ala Gln Leu His Ile Gly Phe Gln Ala Leu
                325                 330                 335

CAC CAG TTC TGT GCT CAG CAT GGC CGG CCA CCT CGG CCC CGC AAT GAG     1056
```

```
His Gln Phe Cys Ala Gln His Gly Arg Pro Pro Arg Pro Arg Asn Glu
            340                 345                 350

GAG GAT GCA GCA GAA CTG GTA GCC TTA GCA CAG GCT GTG AAT GCT CGA   1104
Glu Asp Ala Ala Glu Leu Val Ala Leu Ala Gln Ala Val Asn Ala Arg
        355                 360                 365

GCC CTG CCA GCA GTG CAG CAA AAT AAC CTG GAC GAG GAC CTC ATC CGG   1152
Ala Leu Pro Ala Val Gln Gln Asn Asn Leu Asp Glu Asp Leu Ile Arg
    370                 375                 380

AAG CTG GCA TAT GTG GCT GCT GGG GAT CTG GCA CCC ATA AAC GCC TTC   1200
Lys Leu Ala Tyr Val Ala Ala Gly Asp Leu Ala Pro Ile Asn Ala Phe
385                 390                 395                 400

ATT GGG GGC CTG GCT GCC CAG GAA GTC ATG AAG GCC TGC TCC GGG AAG   1248
Ile Gly Gly Leu Ala Ala Gln Glu Val Met Lys Ala Cys Ser Gly Lys
                405                 410                 415

TTC ATG CCC ATC ATG CAG TGG CTA TAC TTT GAT GCC CTT GAG TGT CTC   1296
Phe Met Pro Ile Met Gln Trp Leu Tyr Phe Asp Ala Leu Glu Cys Leu
            420                 425                 430

CCT GAG GAC AAA GAG GTC CTC ACA GAG GAC AAG TGC CTC CAG CGC CAG   1344
Pro Glu Asp Lys Glu Val Leu Thr Glu Asp Lys Cys Leu Gln Arg Gln
        435                 440                 445

AAC CGT TAT GAC GGG CAA GTG GCT GTG TTT GGC TCA GAC CTG CAA GAG   1392
Asn Arg Tyr Asp Gly Gln Val Ala Val Phe Gly Ser Asp Leu Gln Glu
    450                 455                 460

AAG CTG GGC AAG CAG AAG TAT TTC CTG GTG GGT GCG GGG GCC ATT GGC   1440
Lys Leu Gly Lys Gln Lys Tyr Phe Leu Val Gly Ala Gly Ala Ile Gly
465                 470                 475                 480

TGT GAG CTG CTC AAG AAC TTT GCC ATG ATT GGG CTG GGC TGC GGG GAG   1488
Cys Glu Leu Leu Lys Asn Phe Ala Met Ile Gly Leu Gly Cys Gly Glu
                485                 490                 495

GGT GGA GAA ATC ATC GTT ACA GAC ATG GAC ACC ATT GAG AAG TCA AAT   1536
Gly Gly Glu Ile Ile Val Thr Asp Met Asp Thr Ile Glu Lys Ser Asn
            500                 505                 510

CTG AAT CGA CAG TTT CTT TTC CGG CCC TGG GAT GTC ACG AAG TTA AAG   1584
Leu Asn Arg Gln Phe Leu Phe Arg Pro Trp Asp Val Thr Lys Leu Lys
        515                 520                 525

TCT GAC ACG GCT GCT GCA GCT GTG CGC CAA ATG AAT CCA CAT ATC CGG   1632
Ser Asp Thr Ala Ala Ala Ala Val Arg Gln Met Asn Pro His Ile Arg
    530                 535                 540

GTG ACA AGC CAC CAG AAC CGT GTG GGT CCT GAC ACG GAG CGC ATC TAT   1680
Val Thr Ser His Gln Asn Arg Val Gly Pro Asp Thr Glu Arg Ile Tyr
545                 550                 555                 560

GAT GAC GAT TTT TTC CAA AAC CTA GAT GGC GTG GCC AAT GCC CTG GAC   1728
Asp Asp Asp Phe Phe Gln Asn Leu Asp Gly Val Ala Asn Ala Leu Asp
                565                 570                 575
```

```
AAC GTG GAT GCC CGC ATG TAC ATG GAC CGC CGC TGT GTC TAC TAC CGG      1776
Asn Val Asp Ala Arg Met Tyr Met Asp Arg Arg Cys Val Tyr Tyr Arg
            580                 585                 590

AAG CCA CTG CTG GAG TCA GGC ACA CTG GGC ACC AAA GGC AAT GTG CAG      1824
Lys Pro Leu Leu Glu Ser Gly Thr Leu Gly Thr Lys Gly Asn Val Gln
        595                 600                 605

GTG GTG ATC CCC TTC CTG ACA GAG TCG TAC AGT TCC AGC CAG GAC CCA      1872
Val Val Ile Pro Phe Leu Thr Glu Ser Tyr Ser Ser Ser Gln Asp Pro
    610                 615                 620

CCT GAG AAG TCC ATC CCC ATC TGT ACC CTG AAG AAC TTC CCT AAT GCC      1920
Pro Glu Lys Ser Ile Pro Ile Cys Thr Leu Lys Asn Phe Pro Asn Ala
625                 630                 635                 640

ATC GAG CAC ACC CTG CAG TGG GCT CGG GAT GAG TTT GAA GGC CTC TTC      1968
Ile Glu His Thr Leu Gln Trp Ala Arg Asp Glu Phe Glu Gly Leu Phe
                645                 650                 655

AAG CAG CCA GCA GAA AAT GTC AAC CAG TAC CTC ACA GAC CCC AAG TTT      2016
Lys Gln Pro Ala Glu Asn Val Asn Gln Tyr Leu Thr Asp Pro Lys Phe
            660                 665                 670

GTG GAG CGA ACA CTG CGG CTG GCA GGC ACT CAG CCC TTG GAG GTG CTG      2064
Val Glu Arg Thr Leu Arg Leu Ala Gly Thr Gln Pro Leu Glu Val Leu
        675                 680                 685

GAG GCT GTG CAG CGC AGC CTG GTG CTG CAG CGA CCA CAG ACC TGG GCT      2112
Glu Ala Val Gln Arg Ser Leu Val Leu Gln Arg Pro Gln Thr Trp Ala
    690                 695                 700

GAC TGC GTG ACC TGG GCC TGC CAC CAC TGG CAC ACC CAG TAC TCG AAC      2160
Asp Cys Val Thr Trp Ala Cys His His Trp His Thr Gln Tyr Ser Asn
705                 710                 715                 720

AAC ATC CGG CAG CTG CTG CAC AAC TTC CCT CCT GAC CAG CTC ACA AGC      2208
Asn Ile Arg Gln Leu Leu His Asn Phe Pro Pro Asp Gln Leu Thr Ser
                725                 730                 735

TCA GGA GCG CCG TTC TGG TCT GGG CCC AAA CGC TGT CCA CAC CCG CTC      2256
Ser Gly Ala Pro Phe Trp Ser Gly Pro Lys Arg Cys Pro His Pro Leu
            740                 745                 750

ACC TTT GAT GTC AAC AAT CCC CTG CAT CTG GAC TAT GTG ATG GCT GCT      2304
Thr Phe Asp Val Asn Asn Pro Leu His Leu Asp Tyr Val Met Ala Ala
        755                 760                 765

GCC AAC CTG TTT GCC CAG ACC TAC GGG CTG ACA GGC TCT CAG GAC CGA      2352
Ala Asn Leu Phe Ala Gln Thr Tyr Gly Leu Thr Gly Ser Gln Asp Arg
    770                 775                 780

GCT GCT GTG GCC ACA TTC CTG CAG TCT GTG CAG GTC CCC GAA TTC ACC      2400
Ala Ala Val Ala Thr Phe Leu Gln Ser Val Gln Val Pro Glu Phe Thr
785                 790                 795                 800

CCC AAG TCT GGC GTC AAG ATC CAT GTT TCT GAC CAG GAG CTG CAG AGC      2448
```

```
Pro Lys Ser Gly Val Lys Ile His Val Ser Asp Gln Glu Leu Gln Ser
                805                 810                 815

GCC AAT GCC TCT GTT GAT GAC AGT CGT CTA GAG GAG CTC AAA GCC ACT      2496
Ala Asn Ala Ser Val Asp Asp Ser Arg Leu Glu Glu Leu Lys Ala Thr
            820                 825                 830

CTG CCC AGC CCA GAC AAG CTC CCT GGA TTC AAG ATG TAC CCC ATT GAC      2544
Leu Pro Ser Pro Asp Lys Leu Pro Gly Phe Lys Met Tyr Pro Ile Asp
        835                 840                 845

TTT GAG AAG GAT GAT GAC AGC AAC TTT CAT ATG GAT TTC ATC GTG GCT      2592
Phe Glu Lys Asp Asp Asp Ser Asn Phe His Met Asp Phe Ile Val Ala
    850                 855                 860

GCA TCC AAC CTC CGG GCA GAA AAC TAT GAC ATT CCT TCT GCA GAC CGG      2640
Ala Ser Asn Leu Arg Ala Glu Asn Tyr Asp Ile Pro Ser Ala Asp Arg
865                 870                 875                 880

CAC AAG AGC AAG CTG ATT GCA GGG AAG ATC ATC CCA GCC ATT GCC ACG      2688
His Lys Ser Lys Leu Ile Ala Gly Lys Ile Ile Pro Ala Ile Ala Thr
                885                 890                 895

ACC ACA GCA GCC GTG GTT GGC CTT GTG TGT CTG GAA CTG TAC AAG GTT      2736
Thr Thr Ala Ala Val Val Gly Leu Val Cys Leu Glu Leu Tyr Lys Val
            900                 905                 910

GTG CAG GGG CAC CGA CAG CTT GAC TCC TAC AAG AAT GGT TTC CTC AAC      2784
Val Gln Gly His Arg Gln Leu Asp Ser Tyr Lys Asn Gly Phe Leu Asn
        915                 920                 925

TTG GCC CTG CCT TTC TTT GGT TTC TCT GAA CCC CTT GCC GCA CCA CGT      2832
Leu Ala Leu Pro Phe Phe Gly Phe Ser Glu Pro Leu Ala Ala Pro Arg
    930                 935                 940

CAC CAG TAC TAT AAC CAA GAG TGG ACA TTG TGG GAT CGC TTT GAG GTA      2880
His Gln Tyr Tyr Asn Gln Glu Trp Thr Leu Trp Asp Arg Phe Glu Val
945                 950                 955                 960

CAA GGG CTG CAG CCT AAT GGT GAG GAG ATG ACC CTC AAA CAG TTC CTC      2928
Gln Gly Leu Gln Pro Asn Gly Glu Glu Met Thr Leu Lys Gln Phe Leu
                965                 970                 975

GAC TAT TTT AAG ACA GAG CAC AAA TTA GAG ATC ACC ATG CTG TCC CAG      2976
Asp Tyr Phe Lys Thr Glu His Lys Leu Glu Ile Thr Met Leu Ser Gln
            980                 985                 990

GGC GTG TCC ATG CTC TAT TCC TTC TTC ATG CCA GCT GCC AAG CTC AAG      3024
Gly Val Ser Met Leu Tyr Ser Phe Phe Met Pro Ala Ala Lys Leu Lys
        995                 1000                1005

GAA CGG TTG GAT CAG CCG ATG ACA GAG ATT GTG AGC CGT GTG TCG AAG      3072
Glu Arg Leu Asp Gln Pro Met Thr Glu Ile Val Ser Arg Val Ser Lys
    1010                1015                1020

CGA AAG CTG GGC CGC CAC GTG CGG GCG CTG GTG CTT GAG CTG TGC TGT      3120
Arg Lys Leu Gly Arg His Val Arg Ala Leu Val Leu Glu Leu Cys Cys
1025                1030                1035                1040
```

```
AAC GAC GAG AGC GGC GAG GAT GTC GAG GTT CCC TAT GTC CGA TAC ACC      3168
Asn Asp Glu Ser Gly Glu Asp Val Glu Val Pro Tyr Val Arg Tyr Thr
                1045                1050                1055

ATC CGC TG                                                          3177
Ile Arg
```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 459 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
ATG TCG ACC CCG GCC CGG AGG AGG CTC ATG CGG GAT TTC AAG CGG TTA       48
Met Ser Thr Pro Ala Arg Arg Arg Leu Met Arg Asp Phe Lys Arg Leu
 1               5                  10                  15

CAA GAG GAC CCA CCT GTG GGT GTC AGT GGC GCA CCA TCT GAA AAC AAC       96
Gln Glu Asp Pro Pro Val Gly Val Ser Gly Ala Pro Ser Glu Asn Asn
            20                  25                  30

ATC ATG CAG TGG AAT GCA GTT ATA TTT GGA CCA GAA GGG ACA CCT TTT      144
Ile Met Gln Trp Asn Ala Val Ile Phe Gly Pro Glu Gly Thr Pro Phe
        35                  40                  45

GAA GAT GGT ACT TTT AAA CTA GTA ATA GAA TTT TCT GAA GAA TAT CCA      192
Glu Asp Gly Thr Phe Lys Leu Val Ile Glu Phe Ser Glu Glu Tyr Pro
    50                  55                  60

AAT AAA CCA CCA ACT GTT AGG TTT TTA TCC AAA ATG TTT CAT CCA AAT      240
Asn Lys Pro Pro Thr Val Arg Phe Leu Ser Lys Met Phe His Pro Asn
65                  70                  75                  80

GTG TAT GCT GAT GGT AGC ATA TGT TTA GAT ATC CTT CAG AAT CGA TGG      288
Val Tyr Ala Asp Gly Ser Ile Cys Leu Asp Ile Leu Gln Asn Arg Trp
                85                  90                  95

AGT CCA ACA TAT GAT GTA TCT TCT ATC TTA ACA TCA ATT CAG TCT CTG      336
Ser Pro Thr Tyr Asp Val Ser Ser Ile Leu Thr Ser Ile Gln Ser Leu
            100                 105                 110

CTG GAT GAA CCG AAT CCT AAC AGT CCA GCC AAT AGC CAG GCA GCA CAG      384
Leu Asp Glu Pro Asn Pro Asn Ser Pro Ala Asn Ser Gln Ala Ala Gln
        115                 120                 125
```

```
CTT TAT CAG GAA AAC AAA CGA GAA TAT GAG AAA AGA GTT TCG GCC ATT      432
Leu Tyr Gln Glu Asn Lys Arg Glu Tyr Glu Lys Arg Val Ser Ala Ile
    130                 135                 140

GTT GAA CAA AGC TGG AAT GAT TCA TA                                  459
Val Glu Gln Ser Trp Asn Asp Ser
145                 150
```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
ATG GCG CGC TTT GAG GAT CCA ACA CGG CGA CCC TAC AAG CTA CCT GAT      48
Met Ala Arg Phe Glu Asp Pro Thr Arg Arg Pro Tyr Lys Leu Pro Asp
 1               5                  10                  15

CTG TGC ACG GAA CTG AAC ACT TCA CTG CAA GAC ATA GAA ATA ACC TGT      96
Leu Cys Thr Glu Leu Asn Thr Ser Leu Gln Asp Ile Glu Ile Thr Cys
            20                  25                  30

GTA TAT TGC AAG ACA GTA TTG GAA CTT ACA GAG GTA TTT GAA TTT GCA     144
Val Tyr Cys Lys Thr Val Leu Glu Leu Thr Glu Val Phe Glu Phe Ala
        35                  40                  45

TTT AAA GAT TTA TTT GTG GTG TAT AGA GAC AGT ATA CCG CAT GCT GCA     192
Phe Lys Asp Leu Phe Val Val Tyr Arg Asp Ser Ile Pro His Ala Ala
    50                  55                  60

TGC CAT AAA TGT ATA GAT TTT TAT TCT AGA ATT AGA GAA TTA AGA CAT     240
Cys His Lys Cys Ile Asp Phe Tyr Ser Arg Ile Arg Glu Leu Arg His
65                  70                  75                  80

TAT TCA GAC TCT GTG TAT GGA GAC ACA TTG GAA AAA CTA ACT AAC ACT     288
Tyr Ser Asp Ser Val Tyr Gly Asp Thr Leu Glu Lys Leu Thr Asn Thr
                85                  90                  95

GGG TTA TAC AAT TTA TTA ATA AGG TGC CTG CGG TGC CAG AAA CCG TTG     336
Gly Leu Tyr Asn Leu Leu Ile Arg Cys Leu Arg Cys Gln Lys Pro Leu
            100                 105                 110

AAT CCA GCA GAA AAA CTT AGA CAC CTT AAT GAA AAA CGA CGA TTT CAC     384
```

```
Asn Pro Ala Glu Lys Leu Arg His Leu Asn Glu Lys Arg Arg Phe His
        115                 120                 125

AAC ATA GCT GGG CAC TAT AGA GGC CAG TGC CAT TCG TGC TGC AAC CGA      432
Asn Ile Ala Gly His Tyr Arg Gly Gln Cys His Ser Cys Cys Asn Arg
    130                 135                 140

GCA CGA CAG GAA CGA CTC CAA CGA CGC AGA GAA ACA CAA GTA TA           477
Ala Arg Gln Glu Arg Leu Gln Arg Arg Arg Glu Thr Gln Val
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2625 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..2625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
TCA GGA GAA CCT CAG TCT GAC GAC ATT GAA GCT AGC CGA ATG AAG CGA       48
Ser Gly Glu Pro Gln Ser Asp Asp Ile Glu Ala Ser Arg Met Lys Arg
  1               5                  10                  15

GCA GCT GCA AAG CAT CTA ATA GAA CGC TAC TAC CAC CAG TTA ACT GAG       96
Ala Ala Ala Lys His Leu Ile Glu Arg Tyr Tyr His Gln Leu Thr Glu
             20                  25                  30

GGC TGT GGA AAT GAA GCC TGC ACG AAT GAG TTT TGT GCT TCC TGT CCA      144
Gly Cys Gly Asn Glu Ala Cys Thr Asn Glu Phe Cys Ala Ser Cys Pro
         35                  40                  45

ACT TTT CTT CGT ATG GAT AAT AAT GCA GCA GCT ATT AAA GCC CTC GAG      192
Thr Phe Leu Arg Met Asp Asn Asn Ala Ala Ala Ile Lys Ala Leu Glu
     50                  55                  60

CTT TAT AAG ATT AAT GCA AAA CTC TGT GAT CCT CAT CCC TCC AAG AAA      240
Leu Tyr Lys Ile Asn Ala Lys Leu Cys Asp Pro His Pro Ser Lys Lys
 65                  70                  75                  80

GGA GCA AGC TCA GCT TAC CTT GAG AAC TCG AAA GGT GCC CCC AAC AAC      288
Gly Ala Ser Ser Ala Tyr Leu Glu Asn Ser Lys Gly Ala Pro Asn Asn
                 85                  90                  95

TCC TGC TCT GAG ATA AAA ATG AAC AAG AAA GGC GCT AGA ATT GAT TTT      336
Ser Cys Ser Glu Ile Lys Met Asn Lys Lys Gly Ala Arg Ile Asp Phe
            100                 105                 110
```

```
AAA GAT GTG ACT TAC TTA ACA GAA GAG AAG GTA TAT GAA ATT CTT GAA      384
Lys Asp Val Thr Tyr Leu Thr Glu Glu Lys Val Tyr Glu Ile Leu Glu
        115                 120                 125

TTA TGT AGA GAA AGA GAG GAT TAT TCC CCT TTA ATC CGT GTT ATT GGA      432
Leu Cys Arg Glu Arg Glu Asp Tyr Ser Pro Leu Ile Arg Val Ile Gly
    130                 135                 140

AGA GTT TTT TCT AGT GCT GAG GCA TTG GTA CAG AGC TTC CGG AAA GTT      480
Arg Val Phe Ser Ser Ala Glu Ala Leu Val Gln Ser Phe Arg Lys Val
145                 150                 155                 160

AAA CAA CAC ACC AAG GAA GAA CTG AAA TCT CTT CAA GCA AAA GAT GAA      528
Lys Gln His Thr Lys Glu Glu Leu Lys Ser Leu Gln Ala Lys Asp Glu
                165                 170                 175

GAC AAA GAT GAA GAT GAA AAG GAA AAA GCT GCA TGT TCT GCT GCT GCT      576
Asp Lys Asp Glu Asp Glu Lys Glu Lys Ala Ala Cys Ser Ala Ala Ala
            180                 185                 190

ATG GAA GAA GAC TCA GAA GCA TCT TCC TCA AGG ATA GGT GAT AGC TCA      624
Met Glu Glu Asp Ser Glu Ala Ser Ser Ser Arg Ile Gly Asp Ser Ser
        195                 200                 205

CAG GGA GAC AAC AAT TTG CAA AAA TTA GGC CCT GAT GAT GTG TCT GTG      672
Gln Gly Asp Asn Asn Leu Gln Lys Leu Gly Pro Asp Asp Val Ser Val
    210                 215                 220

GAT ATT GAT GCC ATT AGA AGG GTC TAC ACC AGA TTG CTC TCT AAT GAA      720
Asp Ile Asp Ala Ile Arg Arg Val Tyr Thr Arg Leu Leu Ser Asn Glu
225                 230                 235                 240

AAA ATT GAA ACT GCC TTT CTC AAT GCA CTT GTA TAT TTG TCA CCT AAC      768
Lys Ile Glu Thr Ala Phe Leu Asn Ala Leu Val Tyr Leu Ser Pro Asn
                245                 250                 255

GTG GAA TGT GAC TTG ACG TAT CAC AAT GTA TAC TCT CGA GAT CCT AAT      816
Val Glu Cys Asp Leu Thr Tyr His Asn Val Tyr Ser Arg Asp Pro Asn
            260                 265                 270

TAT CTG AAT TTG TTC ATT ATC GGA ATG GAG AAT AGA AAT CTC CAC AGT      864
Tyr Leu Asn Leu Phe Ile Ile Gly Met Glu Asn Arg Asn Leu His Ser
        275                 280                 285

CCT GAA TAT CTG GAA ATG GCT TTG CCA TTA TTT TGC AAA GCG ATG AGC      912
Pro Glu Tyr Leu Glu Met Ala Leu Pro Leu Phe Cys Lys Ala Met Ser
    290                 295                 300

AAG CTA CCC CTT GCA GCC CAA GGA AAA CTG ATC AGA CTG TGG TCT AAA      960
Lys Leu Pro Leu Ala Ala Gln Gly Lys Leu Ile Arg Leu Trp Ser Lys
305                 310                 315                 320

TAC AAT GCA GAC CAG ATT CGG AGA ATG ATG GAG ACA TTT CAG CAA CTT     1008
Tyr Asn Ala Asp Gln Ile Arg Arg Met Met Glu Thr Phe Gln Gln Leu
                325                 330                 335

ATT ACT TAT AAA GTC ATA AGC AAT GAA TTT AAC AGT CGA AAT CTA GTG     1056
Ile Thr Tyr Lys Val Ile Ser Asn Glu Phe Asn Ser Arg Asn Leu Val
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                340                 345                 350

AAT GAA TTT AAC AGT CGA AAT CTA GTG AAT GAT GAT GAT GCC ATT GTT      1104
Asn Glu Phe Asn Ser Arg Asn Leu Val Asn Asp Asp Asp Ala Ile Val
        355                 360                 365

GCT GCT TCG AAG TGC TTG AAA ATG GTT TAC TAT GCA AAT GTA GTG GGA      1152
Ala Ala Ser Lys Cys Leu Lys Met Val Tyr Tyr Ala Asn Val Val Gly
    370                 375                 380

GGG GAA GTG GAC ACA AAT CAC AAT GAA GAA GAT GAT GAA GAG CCC ATC      1200
Gly Glu Val Asp Thr Asn His Asn Glu Glu Asp Asp Glu Glu Pro Ile
385                 390                 395                 400

CCT GAG TCC AGC GAG CTG ACA CTT CAG GAA CTT TTG GGA GAA GAA AGA      1248
Pro Glu Ser Ser Glu Leu Thr Leu Gln Glu Leu Leu Gly Glu Glu Arg
                405                 410                 415

AGA AAC AAG AAA GGT CTT CGA GTG GAC CCC CTG GAA ACT GAA CTT GGT      1296
Arg Asn Lys Lys Gly Leu Arg Val Asp Pro Leu Glu Thr Glu Leu Gly
            420                 425                 430

GTT AAA ACC CTG GAT TGT CGA AAA CCA CTT ATC CCT TTT GAA GAG TTT      1344
Val Lys Thr Leu Asp Cys Arg Lys Pro Leu Ile Pro Phe Glu Glu Phe
        435                 440                 445

ATT AAT GAA CCA CTG AAT GAG GTT CTA GAA ATG GAT AAA GAT TAT ACT      1392
Ile Asn Glu Pro Leu Asn Glu Val Leu Glu Met Asp Lys Asp Tyr Thr
    450                 455                 460

TTT TTC AAA GTA GAA ACA GAG AAC AAA TTC TCT TTT ATG ACA TGT CCC      1440
Phe Phe Lys Val Glu Thr Glu Asn Lys Phe Ser Phe Met Thr Cys Pro
465                 470                 475                 480

TTT ATA TTG AAT GCT GTC ACA AAG AAT TTG GGA TTA TAT TAT GAC AAT      1488
Phe Ile Leu Asn Ala Val Thr Lys Asn Leu Gly Leu Tyr Tyr Asp Asn
                485                 490                 495

AGA ATT CGC ATG TAC AGT GAA CGA AGA ATC ACT GTT CTC TAC AGC TTA      1536
Arg Ile Arg Met Tyr Ser Glu Arg Arg Ile Thr Val Leu Tyr Ser Leu
            500                 505                 510

GTT CAA GGA CAG CAG TTG AAT CCA TAT TTG AGA CTC AAA GTT AGA CGT      1584
Val Gln Gly Gln Gln Leu Asn Pro Tyr Leu Arg Leu Lys Val Arg Arg
        515                 520                 525

GAC CAT ATC ATA GAT GAT GCA CTT GTC CGG CTA GAG ATG ATC GCT ATG      1632
Asp His Ile Ile Asp Asp Ala Leu Val Arg Leu Glu Met Ile Ala Met
    530                 535                 540

GAA AAT CCT GCA GAC TTG AAG AAG CAG TTG TAT GTG GAA TTT GAA GGA      1680
Glu Asn Pro Ala Asp Leu Lys Lys Gln Leu Tyr Val Glu Phe Glu Gly
545                 550                 555                 560

GAA CAA GGA GTT GAT GAG GGA GGT GTT TCC AAA GAA TTT TTT CAG CTG      1728
Glu Gln Gly Val Asp Glu Gly Gly Val Ser Lys Glu Phe Phe Gln Leu
                565                 570                 575
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```
GTT GTG GAG GAA ATC TTC AAT CCA GAT ATT GGT ATG TTC ACA TAC GAT      1776
Val Val Glu Glu Ile Phe Asn Pro Asp Ile Gly Met Phe Thr Tyr Asp
            580                 585                 590

GAA TCT ACA AAA TTG TTT TGG TTT AAT CCA TCT TCT TTT GAA ACA GAG      1824
Glu Ser Thr Lys Leu Phe Trp Phe Asn Pro Ser Ser Phe Glu Thr Glu
        595                 600                 605

GGT CAG TTT ACT CTG ATT GGC ATA GTA CTG GGT CTG GCT ATT TAC AAT      1872
Gly Gln Phe Thr Leu Ile Gly Ile Val Leu Gly Leu Ala Ile Tyr Asn
    610                 615                 620

AAC TGT ATA CTG GAT GTA CAT TTT CCC ATG GTT GTC TAC AGG AAG CTA      1920
Asn Cys Ile Leu Asp Val His Phe Pro Met Val Val Tyr Arg Lys Leu
625                 630                 635                 640

ATG GGG AAA AAA GGA CTT TTC GTC GAC TTG GGA GAC TCT CAC CCA GTT      1968
Met Gly Lys Lys Gly Leu Phe Val Asp Leu Gly Asp Ser His Pro Val
                645                 650                 655

CTA TAT CAG AGT TTA AAA GAT TTA TTG GAG TAT GTT GGG AAT GTG GAA      2016
Leu Tyr Gln Ser Leu Lys Asp Leu Leu Glu Tyr Val Gly Asn Val Glu
            660                 665                 670

GAT GAC ATG ATG ATC ACT TTC CAG ATA TCA CAG ACA AAT CTT TTT GGT      2064
Asp Asp Met Met Ile Thr Phe Gln Ile Ser Gln Thr Asn Leu Phe Gly
        675                 680                 685

AAC CCA ATG ATG TAT GAT CTA AAG GAA AAT GGT GAT AAA ATT CCA ATT      2112
Asn Pro Met Met Tyr Asp Leu Lys Glu Asn Gly Asp Lys Ile Pro Ile
    690                 695                 700

ACA AAT GAA AAC AGG AAG GAA TTT GTC AAT CTT TAT TCT GAC TAC ATT      2160
Thr Asn Glu Asn Arg Lys Glu Phe Val Asn Leu Tyr Ser Asp Tyr Ile
705                 710                 715                 720

CTC AAT AAA TCA GTA GAA AAA CAG TTC AAG GCT TTT CGG AGA GGT TTT      2208
Leu Asn Lys Ser Val Glu Lys Gln Phe Lys Ala Phe Arg Arg Gly Phe
                725                 730                 735

CAT ATG GTG ACC AAT GAA TCT CCC TTA AAG TAC TTA TTC AGA CCA GAA      2256
His Met Val Thr Asn Glu Ser Pro Leu Lys Tyr Leu Phe Arg Pro Glu
            740                 745                 750

GAA ATT GAA TTG CTT ATA TGT GGA AGC CGC AAT CTA GAT TTC CAA GCA      2304
Glu Ile Glu Leu Leu Ile Cys Gly Ser Arg Asn Leu Asp Phe Gln Ala
        755                 760                 765

CTA GAA GAA ACT ACA GAA TAT GAC GGT GGC TAT ACC AGG GAC TCT GTT      2352
Leu Glu Glu Thr Thr Glu Tyr Asp Gly Gly Tyr Thr Arg Asp Ser Val
    770                 775                 780

CTG ATT AGG GAG TTC TGG GAA ATC GTT CAT TCA TTT ACA GAT GAA CAG      2400
Leu Ile Arg Glu Phe Trp Glu Ile Val His Ser Phe Thr Asp Glu Gln
785                 790                 795                 800

AAA AGA CTC TTC TTG CAG TTT ACA ACG GGC ACA GAC AGA GCA CCT GTG      2448
Lys Arg Leu Phe Leu Gln Phe Thr Thr Gly Thr Asp Arg Ala Pro Val
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                805                 810                 815

GGA GGA CTA GGA AAA TTA AAG ATG ATT ATA GCC AAA AAT GGC CCA GAC      2496
Gly Gly Leu Gly Lys Leu Lys Met Ile Ile Ala Lys Asn Gly Pro Asp
            820                 825                 830

ACA GAA AGG TTA CCT ACA TCT CAT ACT TGC TTT AAT GTG CTT TTA CTT      2544
Thr Glu Arg Leu Pro Thr Ser His Thr Cys Phe Asn Val Leu Leu Leu
        835                 840                 845

CCG GAA TAC TCA AGC AAA GAA AAA CTT AAA GAG AGA TTG TTG AAG GCC      2592
Pro Glu Tyr Ser Ser Lys Glu Lys Leu Lys Glu Arg Leu Leu Lys Ala
    850                 855                 860

ATC ACG TAT GCC AAA GGA TTT GGC ATG CTG TA                          2625
Ile Thr Tyr Ala Lys Gly Phe Gly Met Leu
865                 870                 875
```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
ATG GAG GAG CCG CAG TCA GAT CCT AGC GTC GAG CCC CCT CTG AGT CAG        48
Met Glu Glu Pro Gln Ser Asp Pro Ser Val Glu Pro Pro Leu Ser Gln
  1               5                  10                  15

GAA ACA TTT TCA GAC CTA TGG AAA CTA CTT CCT GAA AAC AAC GTT CTG        96
Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn Asn Val Leu
            20                  25                  30

TCC CCC TTG CCG TCC CAA GCA ATG GAT GAT TTG ATG CTG TCC CCG GAC       144
Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu Ser Pro Asp
        35                  40                  45

GAT ATT GAA CAA TGG TTC ACT GAA GAC CCA GGT CCA GAT GAA GCT CCC       192
Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro Asp Glu Ala Pro
    50                  55                  60

AGA ATG CCA GAG GCT GCT CCC CCC GTG GCC CCT GCA CCA GCA GCT CCT       240
Arg Met Pro Glu Ala Ala Pro Pro Val Ala Pro Ala Pro Ala Ala Pro
65                  70                  75                  80
```

```
ACA CCG GCG GCC CCT GCA CCA GCC CCC TCC TGG CCC CTG TCA TCT TCT        288
Thr Pro Ala Ala Pro Ala Pro Ala Pro Ser Trp Pro Leu Ser Ser Ser
                 85                  90                  95

GTC CCT TCC CAG AAA ACC TAC CAG GGC AGC TAC GGT TTC CGT CTG GGC        336
Val Pro Ser Gln Lys Thr Tyr Gln Gly Ser Tyr Gly Phe Arg Leu Gly
            100                 105                 110

TTC TTG CAT TCT GGG ACA GCC AAG TCT GTG ACT TGC ACG TAC TCC CCT        384
Phe Leu His Ser Gly Thr Ala Lys Ser Val Thr Cys Thr Tyr Ser Pro
        115                 120                 125

GCC CTC AAC AAG ATG TTT TGC CAA CTG GCC AAG ACC TGC CCT GTG CAG        432
Ala Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln
    130                 135                 140

CTG TGG GTT GAT TCC ACA CCC CCG CCC GGC ACC CGC GTC CGC GCC ATG        480
Leu Trp Val Asp Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met
145                 150                 155                 160

GCC ATC TAC AAG CAG TCA CAG CAC ATG ACG GAG GTT GTG AGG CGC TGC        528
Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys
                165                 170                 175

CCC CAC CAT GAG CGC TGC TCA GAT AGC GAT GGT CTG GCC CCT CCT CAG        576
Pro His His Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln
            180                 185                 190

CAT CTT ATC CGA GTG GAA GGA AAT TTG CGT GTG GAG TAT TTG GAT GAC        624
His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp
        195                 200                 205

AGA AAC ACT TTT CGA CAT AGT GTG GTG GTG CCC TAT GAG CCG CCT GAG        672
Arg Asn Thr Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu
    210                 215                 220

GTT GGC TCT GAC TGT ACC ACC ATC CAC TAC AAC TAC ATG TGT AAC AGT        720
Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser
225                 230                 235                 240

TCC TGC ATG GGC GGC ATG AAC CGG AGG CCC ATC CTC ACC ATC ATC ACA        768
Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr
                245                 250                 255

CTG GAA GAC TCC AGT GGT AAT CTA CTG GGA CGG AAC AGC TTT GAG GTG        816
Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val
            260                 265                 270

CGT GTT TGT GCC TGT CCT GGG AGA GAC CGG CGC ACA GAG GAA GAG AAT        864
Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn
        275                 280                 285

CTC CGC AAG AAA GGG GAG CCT CAC CAC GAG CTG CCC CCA GGG AGC ACT        912
Leu Arg Lys Lys Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr
    290                 295                 300

AAG CGA GCA CTG CCC AAC AAC ACC AGC TCC TCT CCC CAG CCA AAG AAG        960
Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys
```

```
305                 310                 315                 320

AAA CCA CTG GAT GGA GAA TAT TTC ACC CTT CAG ATC CGT GGG CGT GAG      1008
Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu
                325                 330                 335

CGC TTC GAG ATG TTC CGA GAG CTG AAT GAG GCC TTG GAA CTC AAG GAT      1056
Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp
            340                 345                 350

GCC CAG GCT GGG AAG GAG CCA GGG GGG AGC AGG GCT CAC TCC AGC CAC      1104
Ala Gln Ala Gly Lys Glu Pro Gly Gly Ser Arg Ala His Ser Ser His
        355                 360                 365

CTG AAG TCC AAA AAG GGT CAG TCT ACC TCC CGC CAT AAA AAA CTC ATG      1152
Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met
    370                 375                 380

TTC AAG ACA GAA GGG CCT GAC TCA GAC TG                               1182
Phe Lys Thr Glu Gly Pro Asp Ser Asp
385                 390
```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 897 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
ATT GCG GCG GCG CCA GAG CTG CTG GAG CGC TCG GGG TCC CCG GGC GGC        48
Ile Ala Ala Ala Pro Glu Leu Leu Glu Arg Ser Gly Ser Pro Gly Gly
  1               5                  10                  15

GGC GGC GGC GCA GAG GAG GAG GCA GGC GGC GGC CCC GGT GGC TCC CCC        96
Gly Gly Gly Ala Glu Glu Glu Ala Gly Gly Gly Pro Gly Gly Ser Pro
            20                  25                  30

CCG GAC GGT GCG CGG CCC GGC CCG TCT CGC GAA CTC GCG GTG GTC GCG       144
Pro Asp Gly Ala Arg Pro Gly Pro Ser Arg Glu Leu Ala Val Val Ala
        35                  40                  45

CGG CCC CGC GCT GCT CCG ACC CCG GGC CCC TCC GCC GCC GCC ATG GCT       192
Arg Pro Arg Ala Ala Pro Thr Pro Gly Pro Ser Ala Ala Ala Met Ala
    50                  55                  60

CGG CCG CTA GTG CCC AGC TCG CAG AAG GCG CTG CTG CTG GAG CTC AAG       240
Arg Pro Leu Val Pro Ser Ser Gln Lys Ala Leu Leu Leu Glu Leu Lys
```

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 65                  70                  75                  80

GGG CTG CAG GAA GAG CCG GTC GAG GGA TTC CGC GTG ACA CTG GTG GAC      288
Gly Leu Gln Glu Glu Pro Val Glu Gly Phe Arg Val Thr Leu Val Asp
                 85                  90                  95

GAG GGC GAT CTA TAC AAC TGG GAG GTG GCC ATT TTC GGG CCC CCC AAC      336
Glu Gly Asp Leu Tyr Asn Trp Glu Val Ala Ile Phe Gly Pro Pro Asn
            100                 105                 110

ACC TAC TAC GAG GGC GGC TAC TTC AAG GCG CGC CTC AAG TTC CCC ATC      384
Thr Tyr Tyr Glu Gly Gly Tyr Phe Lys Ala Arg Leu Lys Phe Pro Ile
        115                 120                 125

GAC TAC CCA TAC TCT CCA CCA GCC TTT CGG TTC CTG ACC AAG ATG TGG      432
Asp Tyr Pro Tyr Ser Pro Pro Ala Phe Arg Phe Leu Thr Lys Met Trp
    130                 135                 140

CAC CCT AAC ATC TAC GAG ACG GGG GAC GTG TGT ATC TCC ATC CTC CAC      480
His Pro Asn Ile Tyr Glu Thr Gly Asp Val Cys Ile Ser Ile Leu His
145                 150                 155                 160

CCG CCG GTG GAC GAC CCC CAG AGC GGG GAG CTG CCC TCA GAG AGG TGG      528
Pro Pro Val Asp Asp Pro Gln Ser Gly Glu Leu Pro Ser Glu Arg Trp
                165                 170                 175

AAC CCC ACG CAG AAC GTC AGG ACC ATT CTC CTG AGT GTG ATC TCC CTC      576
Asn Pro Thr Gln Asn Val Arg Thr Ile Leu Leu Ser Val Ile Ser Leu
            180                 185                 190

CTG AAC GAG CCC AAC ACC TTC TCG CCC GCA AAC GTG GAC GCC TCC GTG      624
Leu Asn Glu Pro Asn Thr Phe Ser Pro Ala Asn Val Asp Ala Ser Val
        195                 200                 205

ATG TAC AGG AAG TGG AAA GAG AGC AAG GGG AAG GAT CGG GAG TAC ACA      672
Met Tyr Arg Lys Trp Lys Glu Ser Lys Gly Lys Asp Arg Glu Tyr Thr
    210                 215                 220

GAC ATC ATC CGG AAG CAG GTC CTG GGG ACC AAG GTG GAC GCG GAG CGT      720
Asp Ile Ile Arg Lys Gln Val Leu Gly Thr Lys Val Asp Ala Glu Arg
225                 230                 235                 240

GAC GGC GTG AAG GTG CCC ACC ACG CTG GCC GAG TAC TGC GTG AAG ACC      768
Asp Gly Val Lys Val Pro Thr Thr Leu Ala Glu Tyr Cys Val Lys Thr
                245                 250                 255

AAG GCG CCG GCG CCC GAC GAG GGC TCA GAC CTC TTC TAC GAC GAC TAC      816
Lys Ala Pro Ala Pro Asp Glu Gly Ser Asp Leu Phe Tyr Asp Asp Tyr
            260                 265                 270

TAC GAG GAC GGC GAG GTG GAG GAG GAG GCC GAC AGC TGC TTC GGG GAC      864
Tyr Glu Asp Gly Glu Val Glu Glu Glu Ala Asp Ser Cys Phe Gly Asp
        275                 280                 285

GAT GAG GAT GAC TCT GGC ACG GAG GAG TCC TGA                          897
Asp Glu Asp Asp Ser Gly Thr Glu Glu Ser
    290                 295
```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CTACTAATAG GTAGAAGCGG TGG 23

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGTAAACCAA AGCACCGACA GGG 23

CLAIMS:

1. An assay for identifying an inhibitor of ubiquitin-mediated proteolysis of a cell-cycle regulatory protein, comprising:
   (i) providing a ubiquitin-conjugating system, comprising a reconstituted protein mixture including the regulatory protein and ubiquitin, under conditions which promote ubiquitination of the regulatory protein;
   (ii) contacting the ubiquitin-conjugating system with a candidate agent;
   (iii) measuring a level of ubiquitination of the regulatory protein in the presence of the candidate agent; and
   (iv) comparing the measured level of ubiquitination in the presence of the candidate agent with a level of ubiquitination of the regulatory protein in the absence of the candidate agent,

   wherein a decrease in ubiquitination of the regulatory protein in the presence of the candidate agent is indicative of an inhibitor of ubiquitination of the regulatory protein.

2. The assay of claim 1, wherein the regulatory protein is selected from a group consisting of p53, $p27^{kip1}$, myc, MATα2, a cyclin, and fos.

3. The assay of claim 1, wherein the ubiquitin is provided in a form selected from a group consisting of:
   (i) an unconjugated ubiquitin, in which case the ubiquitin-conjugating system further comprises an E1 ubiquitin-activating enzyme (E1), an E2 ubiquitin-conjugating enzyme (E2), and adenosine triphosphate;
   (ii) an activated E1:ubiquitin complex, in which case the ubiquitin-conjugating system further comprises an E2; and
   (iii) an activated E2:ubiquitin complex.

4. The assay of claim 1, wherein the reconstituted protein mixture further comprises an E3 ubiquitin-ligase protein.

5. The assay of claim 1, wherein at least one of the ubiquitin and the regulatory protein comprises a detectable label, and the level of ubiquitin-conjugated regulatory protein is quantified by detecting the label in at least one of the regulatory protein, the ubiquitin, and ubiquitin-conjugated regulatory.

6. The method of claim 5, wherein the label group is selected from a group consisting of radioisotopes, fluorescent compounds, enzymes, and enzyme co-factors.

7. The assay of claim 5, wherein the detectable label is a protein having a measurable activity, and the regulatory protein is fusion protein including the detectable label.

8. The assay of claim 1, wherein the amount of ubiquitin-conjugated regulatory protein is quantified by an immunoassay.

9. An assay for identifying an inhibitor of ubiquitin-mediated proteolysis of p53, comprising:
   (i) providing a eukaryotic cell expressing an papillomavirus E6 protein and harboring a reporter gene under transcriptional control of a p53 responsive element;
   (ii) contacting the cell with a candidate agent;
   (iii) measuring the level of expression of the reporter gene in the presence of the candidate agent; and
   (iv) comparing the measured level of ubiquitination in the presence of the candidate agent with a level of ubiquitination of p53 in the absence of the candidate agent,

   wherein a decrease in ubiquitination of the p53 protein in the presence of the candidate agent is indicative of an inhibitor of ubiquitination of the p53 protein.

10. The assay of claim 9, wherein the E6 protein is from a high-risk human papillomavirus.

11. The assay of claim 10, wherein the high-risk human papillomaviruses is selected from a group consisting of HPV-16, HPV-18 and HPV-33.

12. An assay for identifying an inhibitor of E6-mediated degradation of p53, comprising:
   (i) providing an *in vitro* ubiquitin-conjugating system comprising a reconstituted protein mixture including an E6 protein from a human papillomavirus, a p53 protein, adenosine triphosphate, an E1 ubiquitin-activating enzyme, an E2 ubiquitin-conjugating enzyme, and ubiquitin, under conditions wherein the E6 protein mediates ubiquitination of the p53 protein;
   (ii) contacting the ubiquitin-conjugating system with a candidate agent;
   (iii) measuring a level of ubiquitination of the p53 protein in the presence of the candidate agent; and
   (iv) comparing the measured level of ubiquitination in the presence of the candidate agent with a level of ubiquitination of p53 in the absence of the candidate agent,

wherein a decrease in ubiquitination of the p53 protein in the presence of the candidate agent is indicative of an inhibitor of E6-mediated degradation of the p53 protein.

13. The assay of claim 12, wherein the ubiquitin-conjugating system further comprises an E6-AP protein.

14. An assay for identifying an inhibitor of E6-mediated degradation of p53, comprising

i. providing a cell expressing a human papillomavirus E6 protein which mediates ubiquitin-dependent degradation of p53 and results in an impaired p53 cell-cycle checkpoint, wherein the impairment of the p53 cell-cycle checkpoint can cause decreased viability of the cell by facilitating premature progression of the cell through a mitotic cell-cycle under conditions wherein such premature progression results in cell death;

ii. contacting the cell with a candidate agent under conditions wherein the impairment of the p53 cell-cycle checkpoint results in cell death;

iii. measuring a level of viability of the cell in the presence of the candidate agent; and

iv. comparing the level of viability of the cell in the presence of the candidate agent to a level of viability of the cell in the absence of the candidate agent,

wherein an increase in the level of viability in the presence of the candidate agent is indicative of inhibition of the E6-mediated degradation of p53.

15. The assay of claim 14, wherein the conditions under which the impairment of the p53 cell-cycle checkpoint results in cell death comprises exposing the cells to a DNA damaging agent.

16. The assay of claim 15, wherein the DNA damaging agent is γ-radiation.

17. An assay for identifying an inhibitor of ubiquitin-mediated proteolysis of a cell-cycle regulatory protein, comprising:

(i) providing a ubiquitin-conjugating system, including the regulatory protein, ubiquitin and a *UBC* enzyme of SEQ ID No. 2 or 13, under conditions which promote *UBC*-dependent ubiquitination of the regulatory protein;

(ii) contacting the ubiquitin-conjugating system with a candidate agent;

(iii) measuring a level of ubiquitination of the regulatory protein in the presence of the candidate agent; and

(iv) comparing the measured level of ubiquitination in the presence of the candidate agent with a level of ubiquitination of the regulatory protein in the absence of the candidate agent,

wherein a decrease in ubiquitination of the regulatory protein in the presence of the candidate agent is indicative of an inhibitor of ubiquitination of the regulatory protein.

18. The assay of claim 17, wherein the regulatory protein is selected from a group consisting of p53, $p27^{kip1}$, myc, MATα2, a cyclin, and fos.

19. The assay of claim 17, wherein the ubiquitin is provided in a form selected from a group consisting of:

(i) an unconjugated ubiquitin, in which case the ubiquitin-conjugating system further comprises an E1 ubiquitin-activating enzyme (E1) and adenosine triphosphate;

(ii) an activated E1:ubiquitin complex; and

(iii) an activated *UBC*:ubiquitin complex.

20. The assay of claim 17, wherein the reconstituted protein mixture further comprises an E3 ubiquitin-ligase protein.

21. The assay of claim 17, wherein at least one of the ubiquitin and the regulatory protein comprises a detectable label, and the level of ubiquitin-conjugated regulatory protein is quantified by detecting the label in at least one of the regulatory protein, the ubiquitin, and a ubiquitin-conjugated regulatory protein.

22. A substantially pure preparation of an hUCE polypeptide, or a fragment thereof, having an amino acid sequence at least 90% homologous to SEQ ID NO. 2.

23. The polypeptide of claim 22, wherein said polypeptide includes at least 4 consecutive amino acids between residues 107 and 147 of SEQ ID No. 2.

24. The polypeptide of claim 22, having an amino acid sequence at least 95% homologous to the amino acid sequence of SEQ ID No. 2.

25. The polypeptide of claim 22, wherein said polypeptide functions in one of either role of an agonist of cell-cycle regulation or an antagonist of cell-cycle regulation.

26. The polypeptide of claim 25, wherein said polypeptide mediates ubiquitination of a p53 protein.

27. The polypeptide of claim 25, wherein said polypeptide contains at least one amino acid residue different from SEQ ID No. 2 and which inhibits ubiquitination of a p53 protein by an enzyme having a sequence identical to SEQ ID No. 2.

28. The polypeptide of claim 22, which specifically binds at least one of ubiquitin, an E1 enzyme, an E6-AP protein, a papillomavirus E6 protein, or p53.

29. An immunogen comprising the polypeptide of claim 22, in an immunogenic preparation, said immunogen being capable of eliciting an immune response specific for said ubiquitin conjugating enzyme polypeptide.

30. An antibody preparation specifically reactive with an epitope of the polypeptide of claim 22.

31. A substantially pure preparation of an rapUBC polypeptide, or a fragment thereof, having an amino acid sequence at least 80% homologous to SEQ ID NO. 13.

32. The polypeptide of claim 31, wherein said polypeptide functions in one of either role of an agonist of cell-cycle regulation or an antagonist of cell-cycle regulation.

33. The polypeptide of claim 31, wherein said polypeptide contains at least one amino acid residue different from SEQ ID No. 13 and which inhibits ubiquitination by an enzyme having a sequence identical to SEQ ID No. 13.

34. An immunogen comprising the polypeptide of claim 31, in an immunogenic preparation, said immunogen being capable of eliciting an immune response specific for said rapUBC polypeptide.

35. An antibody preparation specifically reactive with an epitope of the polypeptide of claim 31.

36. A substantially pure preparation of a *candida* UbCE polypeptide, or a fragment thereof, having an amino acid sequence at least 90% homologous to SEQ ID NO. 4.

37. An antibody preparation specifically reactive with an epitope of the polypeptide of claim 36.

38. A substantially pure preparation of a *Schizosaccharomyces* UbCE polypeptide, or a fragment thereof, having an amino acid sequence at least 90% homologous to SEQ ID NO. 6.

39. An antibody preparation specifically reactive with an epitope of the polypeptide of claim 38.

40. A recombinant hUbCE polypeptide, or a fragment thereof, having an amino acid sequence at least 90% homologous to SEQ ID NO. 2.

41. The polypeptide of claim 40, which hUbCE polypeptide includes at least 4 consecutive amino acids between residues 107 and 147 of SEQ ID No. 2.

42. The polypeptide of claim 40, having an amino acid sequence represented by the general formula of SEQ ID No. 7.

43. The polypeptide of claim 40, wherein said hUbCE polypeptide functions in one of either role of an agonist of cell-cycle regulation or an antagonist of cell-cycle regulation.

44. The polypeptide of claim 43, wherein said hUbCE polypeptide mediates ubiquitination of a p53 protein.

45. The polypeptide of claim 43, wherein said hUbCE polypeptide contains at least one amino acid residue different from SEQ ID No. 2 and which inhibits ubiquitination of a p53 protein by an enzyme having a sequence identical with SEQ ID No. 2.

46. The polypeptide of claim 45, wherein said hUbCE polypeptide has a ubiquitin conjugating acitivity which is less than 5 percent of a ubiquitin conjugating enzyme identical to SEQ ID No. 2.

47. The polypeptide of claim 40, which specifically binds at least one of ubiquitin, an E1 enzyme, an E6-AP protein, a papillomavirus E6 protein, or p53.

48. The polypeptide of claim 40, wherein said hUbCE polypeptide is a fusion protein further comprising a second polypeptide portion having an amino acid sequence from a protein unrelated to the protein of SEQ ID No. 2.

49. The polypeptide of claim 48, wherein said fusion protein is functional in a two-hybrid assay.

50. A recombinant ubiquitin conjugating enzyme polypeptide, or a fragment thereof, having an amino acid sequence at least 90% homologous to at least one of SEQ ID Nos. 2, 4, 6 or 7.

51. A recombinant rapUBC polypeptide, or a fragment thereof, having an amino acid sequence at least 80% homologous to SEQ ID NO. 13.

52. The polypeptide of claim 51, wherein said rapUBC polypeptide functions in one of either role of an agonist of cell-cycle regulation or an antagonist of cell-cycle regulation.

53. The polypeptide of claim 52, wherein said rapUBC polypeptide mediates ubiquitination of a p53 protein.

54. The polypeptide of claim 52, wherein said rapUBC polypeptide has a ubiquitin conjugating acitivity which is less than 5 percent of a ubiquitin conjugating enzyme identical to SEQ ID No. 13.

55. The polypeptide of claim 40, wherein said rapUBC polypeptide is a fusion protein further comprising a second polypeptide portion having an amino acid sequence from a protein unrelated to the protein of SEQ ID No. 13.

56. The polypeptide of claim 55, wherein said fusion protein is functional in a two-hybrid assay.

57. A substantially pure nucleic acid having a nucleotide sequence which encodes a ubiquitin conjugating enzyme, or a fragment thereof, having an amino acid sequence at least 90% homologous to SEQ ID NO. 2.

58. The nucleic acid of claim 57, wherein said ubiquitin conjugating enzyme specifically binds at least one of ubiquitin, an E1 enzyme, an E6-AP protein, a papillomavirus E6 protein, or p53.

59. The nucleic acid of claim 57, wherein said ubiquitin conjugating enzyme includes at least 4 consecutive amino acids between residues 107 and 147 of SEQ ID No. 2.

60. The nucleic acid of claim 57, wherein said polypeptide encoded by said nucleic acid functions in one of either role of an agonist of cell cycle regulation or an antagonist of cell cycle regulation.

61. The nucleic acid of claim 60, wherein said polypeptide encoded by said nucleic acid mediates ubiquitination of a p53 protein.

62. The nucleic acid of claim 60, wherein said polypeptide encoded by said nucleic acid has a ubiquitin conjugating acitivity which is less than 5 percent of a ubiquitin conjugating enzyme identical to SEQ ID No. 2, which polypeptide antagonizes ubiquitination mediated by an enzyme identical to SEQ ID NO. 2.

63. The nucleic acid of claim 57, wherein said nucleotide sequence hybridizes under stringent conditions to a nucleic acid probe corresponding to at least 12 consecutive nucleotides of SEQ ID No. 1.

64. A substantially pure nucleic acid having a nucleotide sequence which encodes a ubiquitin conjugating enzyme, or a fragment thereof, having an amino acid sequence at least 80% homologous to SEQ ID NO. 13.

65. The nucleic acid of claim 64, wherein said polypeptide encoded by said nucleic acid functions in one of either role of an agonist of cell cycle regulation or an antagonist of cell cycle regulation.

66. The nucleic acid of claim 64, wherein said nucleotide sequence hybridizes under stringent conditions to a nucleic acid probe corresponding to at least 12 consecutive nucleotides of SEQ ID No. 1.

67. The nucleic acid of claim 57 or 64, further comprising a transcriptional regulatory sequence operably linked to said nucleotide sequence so as to render said nucleotide sequence suitable for use as an expression vector.

68. An expression vector, capable of replicating in at least one of a prokaryotic cell and eukaryotic cell, comprising the nucleic acid of claim 57 or 64.

69. A host cell transfected with the expression vector of claim 68 and expressing said polypeptide.

70. A method of producing a recombinant ubiquitin conjugating enzyme comprising culturing the cell of claim 69 in a cell culture medium to express said ubiquitin conjugating enzyme and isolating said ubiquitin conjugating enzyme from said cell culture.

71. A transgenic animal comprising an expressible form of the nucleic acid of claim 57 or 64.

72. A transgenic animal in which at least one copy a gene homolgous to the UbCE gene of SEQ ID No. 1 has been disrupted.

73. A transgenic animal in which at least one copy a gene homolgous to the rapUBC gene of SEQ ID No. 12 has been disrupted.

74. A substantially pure nucleic acid having a nucleotide sequence which encodes a ubiquitin conjugating enzyme, or a fragment thereof, having an amino acid sequence at least 90% homologous to at least one of SEQ ID Nos. 2, 4 or 6.

75. A recombinant gene comprising a UBC-encoding nucleotide sequence at least 90% homologous to one of SEQ ID Nos. 1, 3 or 5, or a fragment thereof, said nucleotide sequence operably linked to a transcriptional regulatory sequence in an open reading frame and translatable to a polypeptide capable of functioning in one of either role of an agonist of cell cycle regulation or an antagonist of cell cycle regulation.

76. The recombinant gene of claim 75, which is derived from a genomic clone and optionally includes intronic nucleotide sequences disrupting said UBC-encoding nucleotide sequence.

77. The recombinant gene of claim 75, wherein said recombinant gene is functional in a two-hybrid assay.

78. A probe/primer comprising a substantially purified oligonucleotide, said oligonucleotide containing a region of nucleotide sequence which hybridizes under stringent conditions to at least 10 consecutive nucleotides of sense or antisense sequence of at least one of SEQ ID Nos. 1, 3, 5 or 12 or naturally occuring mutants thereof.

79. The probe/primer of claim 78, further comprising a label group attached thereto and able to be detected.

80. A method of determining if a subject is at risk for a disorder characterized by unwanted cell proliferation, comprising detecting, in a tissue of said subject, the presence or absence of a genetic lesion characterized by at least one of

a mutation of a UBC gene encoding a protein represented by SEQ ID No. 2 or 13, or a homolog thereof; and the mis-expression of said gene.

81. The method of claim 80, wherein detecting said genetic lesion comprises ascertaining the existence of at least one of

i. a deletion of one or more nucleotides from said gene,
ii. an addition of one or more nucleotides to said gene,
iii. an substitution of one or more nucleotides of said gene,
iv. a gross chromosomal rearrangement of said gene.
v. a gross alteration in the level of a messanger RNA transcript of said gene,
vi. the presence of a non-wild type splicing pattern of a messanger RNA transcript of said gene, and
vii. a non-wild type level of said protein.

82. The method of claim 80 wherein detecting said genetic lesion comprises

i. providing a probe/primer comprising an oligonucleotide containing a region of nucleotide sequence which hybridizes to a sense or antisense sequence of SEQ ID No. 1 or 12 or naturally occuring mutants thereof or 5' or 3' flanking sequences naturally associated with said gene;
ii. exposing said probe/primer to nucleic acid of said tissue; and
iii. detecting, by hybridization of said probe/primer to said nucleic acid, the presence or absence of said genetic lesion.

83. The method of claim 80, wherein detecting said lesion comprises utilizing said probe/primer to determine the nucleotide sequence of said gene and, optionally, of said flanking nucleic acid sequences.

84. The method of claim 80, wherein detecting said lesion comprises utilizing said probe/primer to in a polymerase chain reaction (PCR).

85. The method of claim 80, wherein detecting said lesion comprises utilizing said probe/primer in a ligation chain reaction (LCR).

86. The method of claim 81, wherein the level of said protein is detected in an immunoassay.

87. A method for identifying inhibitors of a human ubiquitin-conjugating enzyme (hUCE) comprising:

(i) providing a molecular model of an hUCE including the amino acid residues Cys-85, Leu-86, Asp-87, Ile-88, Arg-90, Ser-91, Leu-109, Asn-114, Asp-116, and Asp-117, the atomic coordinates of said residues, at 300°K, having an overall RMS within 2Å of the atomic coordinates shown in Figure 2,

(ii) providing a molecular model of a candidate drug,

(iii) docking said drug model with said hUCE model and determining binding criteria of the docked models, and

(iv) determining from said binding criteria the likelihood of said candidate drug being an inhibitor of said hUCE.

88. The method of claim 87, wherein said binding criteria is selected from a group consisting of electrostatic interactions, hydrogen bonding, hydrophobic interactions, desolvation effects, cooperative motions of ligand and enzyme, and a combination thereof.

89. The method of claim 87, comprising the further steps of producing said candidate drug.

90. The method of claim 87, comprising the further steps of providing said candidate drug and a protein comprising an amino acid sequence represented by SEQ ID No. 2 in an assay to determine the inhibitory activity of said candidate drug.

91. The method of claim 87, wherein said hUCE model comprises amino acid residues Arg-5 through Met-147 of SEQ ID No. 2, the atomic coordinates of said residues, at 300°K, having an overall RMS within 2Å of the atomic coordinates shown in Figure 1.

92. An electronic memory means having stored therein an addressable electronic representation of atomic coordinates of a molecular model of a human ubiquitin-conjugating enzyme including the amino acid residues Cys-85, Leu-86, Asp-87, Ile-88, Arg-90, Ser-91, Leu-109, Asn-114, Asp-116, and Asp-117, the atomic coordinates of said residues, at 300°K, having an overall RMS within 2Å of the atomic coordinates shown in Figure 2.

93. The electronic memory of claim 92, wherein said human ubiquitin-conjugating enzyme model comprises amino acid residues Arg-5 through Met-147 of SEQ ID No. 2, the atomic coordinates of said residues, at 300°K, having an overall RMS within 2Å of the atomic coordinates shown in Figure 1.

Figure 1

```
ATOM      1  N   ARG 1   5      10.652  30.749  37.986  1.00  0.00
ATOM      2  CA  ARG 1   5      10.674  30.876  39.370  1.00  0.00
ATOM      3  C   ARG 1   5       9.386  31.560  39.753  1.00  0.00
ATOM      4  O   ARG 1   5       9.153  32.661  39.298  1.00  0.00
ATOM      5  CB  ARG 1   5      11.872  31.683  39.871  1.00  0.00
ATOM      6  CG  ARG 1   5      12.638  31.033  41.051  1.00  0.00
ATOM      7  CD  ARG 1   5      11.956  31.005  42.439  1.00  0.00
ATOM      8  NE  ARG 1   5      11.007  29.919  42.560  1.00  0.00
ATOM      9  CZ  ARG 1   5      10.281  29.677  43.686  1.00  0.00
ATOM     10  NH1 ARG 1   5      10.417  30.413  44.773  1.00  0.00
ATOM     11  NH2 ARG 1   5       9.411  28.694  43.623  1.00  0.00
ATOM     12 1H   ARG 1   5      10.497  29.737  37.803  1.00  0.00
ATOM     13 2H   ARG 1   5       9.927  31.348  37.541  1.00  0.00
ATOM     14 3H   ARG 1   5      11.573  31.167  37.744  1.00  0.00
ATOM     15  HE  ARG 1   5      10.888  29.459  41.680  1.00  0.00
ATOM     16 1HH1 ARG 1   5       9.832  30.497  45.580  1.00  0.00
ATOM     17 2HH1 ARG 1   5      11.297  30.876  44.878  1.00  0.00
ATOM     18 1HH2 ARG 1   5       8.878  28.410  44.420  1.00  0.00
ATOM     19 2HH2 ARG 1   5       9.283  28.223  42.749  1.00  0.00
ATOM     20  N   ILE 1   6       8.510  30.841  40.468  1.00  0.00
ATOM     21  CA  ILE 1   6       7.082  31.170  40.678  1.00  0.00
ATOM     22  C   ILE 1   6       6.442  31.065  39.284  1.00  0.00
ATOM     23  O   ILE 1   6       5.956  29.988  38.915  1.00  0.00
ATOM     24  CB  ILE 1   6       6.853  32.470  41.413  1.00  0.00
ATOM     25  CG1 ILE 1   6       7.651  32.561  42.727  1.00  0.00
ATOM     26  CG2 ILE 1   6       5.366  32.803  41.630  1.00  0.00
ATOM     27  CD1 ILE 1   6       6.834  32.009  43.915  1.00  0.00
ATOM     28  H   ILE 1   6       8.808  29.963  40.841  1.00  0.00
ATOM     29  N   HIS 1   7       6.540  32.257  38.639  1.00  0.00
ATOM     30  CA  HIS 1   7       6.197  32.320  37.173  1.00  0.00
ATOM     31  C   HIS 1   7       7.002  31.274  36.346  1.00  0.00
ATOM     32  O   HIS 1   7       8.174  30.919  36.611  1.00  0.00
ATOM     33  CB  HIS 1   7       6.233  33.740  36.613  1.00  0.00
ATOM     34  CG  HIS 1   7       7.507  34.441  37.147  1.00  0.00
ATOM     35  ND1 HIS 1   7       8.661  34.555  36.453  1.00  0.00
ATOM     36  CD2 HIS 1   7       7.660  35.160  38.373  1.00  0.00
ATOM     37  CE1 HIS 1   7       9.552  35.219  37.259  1.00  0.00
ATOM     38  NE2 HIS 1   7       8.924  35.642  38.428  1.00  0.00
ATOM     39  H   HIS 1   7       7.119  32.928  39.101  1.00  0.00
ATOM     40 1HD  HIS 1   7       8.806  34.258  35.530  1.00  0.00
ATOM     41  N   LYS 1   8       6.366  30.860  35.208  1.00  0.00
ATOM     42  CA  LYS 1   8       6.776  29.679  34.371  1.00  0.00
ATOM     43  C   LYS 1   8       6.529  28.399  35.097  1.00  0.00
ATOM     44  O   LYS 1   8       5.719  27.551  34.809  1.00  0.00
ATOM     45  CB  LYS 1   8       8.237  29.782  33.828  1.00  0.00
ATOM     46  CG  LYS 1   8       8.500  29.320  32.392  1.00  0.00
ATOM     47  CD  LYS 1   8       9.916  29.656  31.893  1.00  0.00
ATOM     48  CE  LYS 1   8       9.996  29.567  30.420  1.00  0.00
ATOM     49  NZ  LYS 1   8      11.060  30.278  29.662  1.00  0.00
ATOM     50  H   LYS 1   8       5.445  31.225  35.069  1.00  0.00
ATOM     51 1HZ  LYS 1   8      10.982  31.309  29.543  1.00  0.00
ATOM     52 2HZ  LYS 1   8      12.021  29.906  29.803  1.00  0.00
ATOM     53 3HZ  LYS 1   8      11.084  30.047  28.648  1.00  0.00
ATOM     54  N   GLU 1   9       7.274  28.215  36.215  1.00  0.00
ATOM     55  CA  GLU 1   9       6.995  27.070  37.159  1.00  0.00
```

Figure 1(con't)

ATOM	56	C	GLU	1	9	5.445	26.859	37.570	1.00	0.00
ATOM	57	O	GLU	1	9	4.977	25.769	37.789	1.00	0.00
ATOM	58	CB	GLU	1	9	7.951	27.203	38.425	1.00	0.00
ATOM	59	CG	GLU	1	9	9.433	26.780	38.565	1.00	0.00
ATOM	60	CD	GLU	1	9	10.169	27.525	39.767	1.00	0.00
ATOM	61	OE1	GLU	1	9	9.570	27.669	40.887	1.00	0.00
ATOM	62	OE2	GLU	1	9	11.354	27.904	39.613	1.00	0.00
ATOM	63	H	GLU	1	9	7.918	28.973	36.320	1.00	0.00
ATOM	64	N	LEU	1	10	4.816	27.970	37.728	1.00	0.00
ATOM	65	CA	LEU	1	10	3.434	28.097	38.068	1.00	0.00
ATOM	66	C	LEU	1	10	3.047	29.230	37.145	1.00	0.00
ATOM	67	O	LEU	1	10	3.769	30.204	37.045	1.00	0.00
ATOM	68	CB	LEU	1	10	3.176	28.409	39.531	1.00	0.00
ATOM	69	CG	LEU	1	10	2.041	27.485	40.074	1.00	0.00
ATOM	70	CD1	LEU	1	10	0.728	27.903	39.503	1.00	0.00
ATOM	71	CD2	LEU	1	10	2.366	26.000	39.832	1.00	0.00
ATOM	72	H	LEU	1	10	5.291	28.782	37.389	1.00	0.00
ATOM	73	N	ASN	1	11	1.850	29.001	36.566	1.00	0.00
ATOM	74	CA	ASN	1	11	1.355	29.849	35.463	1.00	0.00
ATOM	75	C	ASN	1	11	-0.107	30.195	35.375	1.00	0.00
ATOM	76	O	ASN	1	11	-0.745	29.756	34.411	1.00	0.00
ATOM	77	CB	ASN	1	11	2.047	29.486	34.124	1.00	0.00
ATOM	78	CG	ASN	1	11	1.754	30.546	33.096	1.00	0.00
ATOM	79	OD1	ASN	1	11	1.217	31.610	33.377	1.00	0.00
ATOM	80	ND2	ASN	1	11	1.971	30.162	31.811	1.00	0.00
ATOM	81	H	ASN	1	11	1.420	28.167	36.911	1.00	0.00
ATOM	82	1HD2	ASN	1	11	2.285	29.261	31.512	1.00	0.00
ATOM	83	2HD2	ASN	1	11	1.643	30.782	31.098	1.00	0.00
ATOM	84	N	ASP	1	12	-0.619	30.939	36.323	1.00	0.00
ATOM	85	CA	ASP	1	12	-2.064	31.262	36.250	1.00	0.00
ATOM	86	C	ASP	1	12	-2.668	31.635	34.910	1.00	0.00
ATOM	87	O	ASP	1	12	-3.709	31.008	34.539	1.00	0.00
ATOM	88	CB	ASP	1	12	-2.517	32.237	37.409	1.00	0.00
ATOM	89	CG	ASP	1	12	-1.293	32.675	38.157	1.00	0.00
ATOM	90	OD1	ASP	1	12	-0.497	33.446	37.645	1.00	0.00
ATOM	91	OD2	ASP	1	12	-1.057	32.123	39.266	1.00	0.00
ATOM	92	H	ASP	1	12	-0.119	31.179	37.155	1.00	0.00
ATOM	93	N	LEU	1	13	-2.099	32.601	34.132	1.00	0.00
ATOM	94	CA	LEU	1	13	-2.827	33.180	32.995	1.00	0.00
ATOM	95	C	LEU	1	13	-2.951	32.329	31.780	1.00	0.00
ATOM	96	O	LEU	1	13	-3.808	32.567	30.921	1.00	0.00
ATOM	97	CB	LEU	1	13	-2.337	34.600	32.584	1.00	0.00
ATOM	98	CG	LEU	1	13	-3.491	35.515	32.232	1.00	0.00
ATOM	99	CD1	LEU	1	13	-4.133	36.006	33.554	1.00	0.00
ATOM	100	CD2	LEU	1	13	-2.935	36.524	31.217	1.00	0.00
ATOM	101	H	LEU	1	13	-1.276	33.096	34.408	1.00	0.00
ATOM	102	N	ALA	1	14	-2.089	31.252	31.763	1.00	0.00
ATOM	103	CA	ALA	1	14	-2.227	30.131	30.792	1.00	0.00
ATOM	104	C	ALA	1	14	-3.449	29.293	31.048	1.00	0.00
ATOM	105	O	ALA	1	14	-3.724	28.399	30.301	1.00	0.00
ATOM	106	CB	ALA	1	14	-1.062	29.249	30.600	1.00	0.00
ATOM	107	H	ALA	1	14	-1.479	31.103	32.541	1.00	0.00
ATOM	108	N	ARG	1	15	-4.037	29.445	32.285	1.00	0.00
ATOM	109	CA	ARG	1	15	-5.241	28.633	32.573	1.00	0.00
ATOM	110	C	ARG	1	15	-6.478	29.572	32.619	1.00	0.00
ATOM	111	O	ARG	1	15	-7.563	29.184	32.147	1.00	0.00

Figure 1(con't)

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ATOM    112  CB  ARG 1   15      -5.074  27.850  33.877  1.00  0.00
ATOM    113  CG  ARG 1   15      -5.256  26.348  33.808  1.00  0.00
ATOM    114  CD  ARG 1   15      -6.599  25.816  34.374  1.00  0.00
ATOM    115  NE  ARG 1   15      -7.738  26.515  33.767  1.00  0.00
ATOM    116  CZ  ARG 1   15      -8.322  27.475  34.535  1.00  0.00
ATOM    117  NH1 ARG 1   15      -9.426  28.064  34.120  1.00  0.00
ATOM    118  NH2 ARG 1   15      -7.720  27.973  35.652  1.00  0.00
ATOM    119  H   ARG 1   15      -3.720  30.097  32.975  1.00  0.00
ATOM    120  HE  ARG 1   15      -8.062  26.201  32.875  1.00  0.00
ATOM    121 1HH1 ARG 1   15      -9.878  28.795  34.631  1.00  0.00
ATOM    122 2HH1 ARG 1   15      -9.779  27.853  33.209  1.00  0.00
ATOM    123 1HH2 ARG 1   15      -8.137  28.803  36.022  1.00  0.00
ATOM    124 2HH2 ARG 1   15      -6.866  27.700  36.093  1.00  0.00
ATOM    125  N   ASP 1   16      -6.237  30.813  33.067  1.00  0.00
ATOM    126  CA  ASP 1   16      -7.250  31.856  32.803  1.00  0.00
ATOM    127  C   ASP 1   16      -6.824  33.136  32.067  1.00  0.00
ATOM    128  O   ASP 1   16      -6.532  34.221  32.610  1.00  0.00
ATOM    129  CB  ASP 1   16      -8.089  32.302  34.005  1.00  0.00
ATOM    130  CG  ASP 1   16      -8.462  31.097  34.974  1.00  0.00
ATOM    131  OD1 ASP 1   16      -9.602  30.692  34.912  1.00  0.00
ATOM    132  OD2 ASP 1   16      -7.672  30.572  35.769  1.00  0.00
ATOM    133  H   ASP 1   16      -5.451  31.212  33.539  1.00  0.00
ATOM    134  N   PRO 1   17      -6.956  33.072  30.746  1.00  0.00
ATOM    135  CA  PRO 1   17      -6.993  34.342  30.013  1.00  0.00
ATOM    136  C   PRO 1   17      -8.205  35.156  30.521  1.00  0.00
ATOM    137  O   PRO 1   17      -9.305  34.673  30.362  1.00  0.00
ATOM    138  CB  PRO 1   17      -7.265  33.841  28.530  1.00  0.00
ATOM    139  CG  PRO 1   17      -6.733  32.384  28.576  1.00  0.00
ATOM    140  CD  PRO 1   17      -7.148  31.899  29.962  1.00  0.00
ATOM    141  N   PRO 1   18      -7.965  36.355  31.086  1.00  0.00
ATOM    142  CA  PRO 1   18      -9.083  37.138  31.627  1.00  0.00
ATOM    143  C   PRO 1   18      -9.936  37.823  30.552  1.00  0.00
ATOM    144  O   PRO 1   18     -10.510  37.184  29.678  1.00  0.00
ATOM    145  CB  PRO 1   18      -8.415  37.993  32.696  1.00  0.00
ATOM    146  CG  PRO 1   18      -6.972  38.217  32.269  1.00  0.00
ATOM    147  CD  PRO 1   18      -6.703  36.974  31.360  1.00  0.00
ATOM    148  N   ALA 1   19     -10.151  39.105  30.790  1.00  0.00
ATOM    149  CA  ALA 1   19     -11.197  39.768  29.931  1.00  0.00
ATOM    150  C   ALA 1   19     -10.607  40.086  28.534  1.00  0.00
ATOM    151  O   ALA 1   19     -10.127  41.187  28.324  1.00  0.00
ATOM    152  CB  ALA 1   19     -11.617  41.179  30.598  1.00  0.00
ATOM    153  H   ALA 1   19      -9.561  39.653  31.383  1.00  0.00
ATOM    154  N   GLN 1   20     -10.496  39.036  27.758  1.00  0.00
ATOM    155  CA  GLN 1   20      -9.643  38.863  26.552  1.00  0.00
ATOM    156  C   GLN 1   20      -8.342  39.556  26.683  1.00  0.00
ATOM    157  O   GLN 1   20      -8.219  40.714  26.316  1.00  0.00
ATOM    158  CB  GLN 1   20     -10.452  39.059  25.250  1.00  0.00
ATOM    159  CG  GLN 1   20     -11.446  40.245  25.067  1.00  0.00
ATOM    160  CD  GLN 1   20     -12.575  40.215  26.077  1.00  0.00
ATOM    161  OE1 GLN 1   20     -12.883  41.218  26.660  1.00  0.00
ATOM    162  NE2 GLN 1   20     -13.154  39.042  26.289  1.00  0.00
ATOM    163  H   GLN 1   20     -11.149  38.324  28.017  1.00  0.00
ATOM    164 1HE2 GLN 1   20     -12.901  38.240  25.748  1.00  0.00
ATOM    165 2HE2 GLN 1   20     -13.792  38.993  27.058  1.00  0.00
ATOM    166  N   CYS 1   21      -7.381  38.866  27.312  1.00  0.00
ATOM    167  CA  CYS 1   21      -5.983  39.312  27.548  1.00  0.00
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Figure 1(con't)

ATOM	168	C	CYS	1	21	-5.049	38.159	27.644	1.00	0.00
ATOM	169	O	CYS	1	21	-5.488	37.103	28.037	1.00	0.00
ATOM	170	CB	CYS	1	21	-5.939	40.115	28.837	1.00	0.00
ATOM	171	SG	CYS	1	21	-6.547	41.738	28.478	1.00	0.00
ATOM	172	H	CYS	1	21	-7.581	37.909	27.521	1.00	0.00
ATOM	173	N	SER	1	22	-3.768	38.479	27.242	1.00	0.00
ATOM	174	CA	SER	1	22	-2.909	37.373	26.846	1.00	0.00
ATOM	175	C	SER	1	22	-1.484	37.385	27.299	1.00	0.00
ATOM	176	O	SER	1	22	-0.890	38.502	27.246	1.00	0.00
ATOM	177	CB	SER	1	22	-3.010	37.109	25.307	1.00	0.00
ATOM	178	OG	SER	1	22	-4.179	37.764	24.726	1.00	0.00
ATOM	179	H	SER	1	22	-3.415	39.413	27.183	1.00	0.00
ATOM	180	HG	SER	1	22	-3.987	37.872	23.804	1.00	0.00
ATOM	181	N	ALA	1	23	-0.882	36.264	27.816	1.00	0.00
ATOM	182	CA	ALA	1	23	0.449	36.497	28.382	1.00	0.00
ATOM	183	C	ALA	1	23	1.533	35.875	27.516	1.00	0.00
ATOM	184	O	ALA	1	23	1.418	34.935	26.775	1.00	0.00
ATOM	185	CB	ALA	1	23	0.545	35.912	29.743	1.00	0.00
ATOM	186	H	ALA	1	23	-1.458	35.449	27.752	1.00	0.00
ATOM	187	N	GLY	1	24	2.746	36.445	27.787	1.00	0.00
ATOM	188	CA	GLY	1	24	3.850	35.741	27.233	1.00	0.00
ATOM	189	C	GLY	1	24	5.127	36.253	27.699	1.00	0.00
ATOM	190	O	GLY	1	24	5.075	37.310	28.265	1.00	0.00
ATOM	191	H	GLY	1	24	3.000	37.253	28.319	1.00	0.00
ATOM	192	N	PRO	1	25	6.264	35.552	27.463	1.00	0.00
ATOM	193	CA	PRO	1	25	7.528	36.069	27.834	1.00	0.00
ATOM	194	C	PRO	1	25	7.954	37.302	27.064	1.00	0.00
ATOM	195	O	PRO	1	25	7.102	37.967	26.519	1.00	0.00
ATOM	196	CB	PRO	1	25	8.536	34.960	27.498	1.00	0.00
ATOM	197	CG	PRO	1	25	7.766	33.902	26.624	1.00	0.00
ATOM	198	CD	PRO	1	25	6.327	34.297	26.774	1.00	0.00
ATOM	199	N	VAL	1	26	9.251	37.652	27.070	1.00	0.00
ATOM	200	CA	VAL	1	26	9.831	38.466	25.975	1.00	0.00
ATOM	201	C	VAL	1	26	10.054	37.488	24.900	1.00	0.00
ATOM	202	O	VAL	1	26	9.071	36.906	24.424	1.00	0.00
ATOM	203	CB	VAL	1	26	11.032	39.240	26.509	1.00	0.00
ATOM	204	CG1	VAL	1	26	10.726	40.772	26.799	1.00	0.00
ATOM	205	CG2	VAL	1	26	11.723	38.692	27.823	1.00	0.00
ATOM	206	H	VAL	1	26	9.681	37.030	27.724	1.00	0.00
ATOM	207	N	GLY	1	27	11.292	37.168	24.590	1.00	0.00
ATOM	208	CA	GLY	1	27	11.482	35.738	24.271	1.00	0.00
ATOM	209	C	GLY	1	27	11.647	34.818	25.477	1.00	0.00
ATOM	210	O	GLY	1	27	11.513	35.432	26.503	1.00	0.00
ATOM	211	H	GLY	1	27	12.099	37.604	24.988	1.00	0.00
ATOM	212	N	ASP	1	28	12.041	33.489	25.391	1.00	0.00
ATOM	213	CA	ASP	1	28	12.052	32.693	26.625	1.00	0.00
ATOM	214	C	ASP	1	28	12.264	33.254	28.042	1.00	0.00
ATOM	215	O	ASP	1	28	11.812	32.613	29.013	1.00	0.00
ATOM	216	CB	ASP	1	28	12.848	31.459	26.313	1.00	0.00
ATOM	217	CG	ASP	1	28	12.220	30.275	26.971	1.00	0.00
ATOM	218	OD1	ASP	1	28	11.048	29.929	26.718	1.00	0.00
ATOM	219	OD2	ASP	1	28	12.910	29.622	27.780	1.00	0.00
ATOM	220	H	ASP	1	28	12.089	33.023	24.507	1.00	0.00
ATOM	221	N	ASP	1	29	13.052	34.361	28.176	1.00	0.00
ATOM	222	CA	ASP	1	29	13.109	34.931	29.560	1.00	0.00
ATOM	223	C	ASP	1	29	11.716	35.121	30.289	1.00	0.00

Figure 1(con't)

ATOM	224	O	ASP	1	29	10.664	35.488	29.732	1.00	0.00
ATOM	225	CB	ASP	1	29	14.006	36.222	29.650	1.00	0.00
ATOM	226	CG	ASP	1	29	13.724	37.078	30.916	1.00	0.00
ATOM	227	OD1	ASP	1	29	13.034	38.080	30.842	1.00	0.00
ATOM	228	OD2	ASP	1	29	14.208	36.708	31.973	1.00	0.00
ATOM	229	H	ASP	1	29	13.367	34.766	27.317	1.00	0.00
ATOM	230	N	MET	1	30	11.742	34.874	31.593	1.00	0.00
ATOM	231	CA	MET	1	30	10.513	34.871	32.347	1.00	0.00
ATOM	232	C	MET	1	30	10.424	35.967	33.348	1.00	0.00
ATOM	233	O	MET	1	30	9.395	36.073	34.009	1.00	0.00
ATOM	234	CB	MET	1	30	10.024	33.562	32.904	1.00	0.00
ATOM	235	CG	MET	1	30	8.608	33.344	32.660	1.00	0.00
ATOM	236	SD	MET	1	30	8.121	33.393	30.892	1.00	0.00
ATOM	237	CE	MET	1	30	6.473	32.740	31.116	1.00	0.00
ATOM	238	H	MET	1	30	12.645	34.898	32.021	1.00	0.00
ATOM	239	N	PHE	1	31	11.476	36.831	33.387	1.00	0.00
ATOM	240	CA	PHE	1	31	11.426	37.966	34.248	1.00	0.00
ATOM	241	C	PHE	1	31	10.748	39.124	33.639	1.00	0.00
ATOM	242	O	PHE	1	31	10.171	39.983	34.265	1.00	0.00
ATOM	243	CB	PHE	1	31	12.847	38.280	34.753	1.00	0.00
ATOM	244	CG	PHE	1	31	13.502	36.936	35.115	1.00	0.00
ATOM	245	CD1	PHE	1	31	14.835	36.780	34.734	1.00	0.00
ATOM	246	CD2	PHE	1	31	12.856	35.900	35.819	1.00	0.00
ATOM	247	CE1	PHE	1	31	15.477	35.585	34.972	1.00	0.00
ATOM	248	CE2	PHE	1	31	13.540	34.632	36.102	1.00	0.00
ATOM	249	CZ	PHE	1	31	14.843	34.454	35.587	1.00	0.00
ATOM	250	H	PHE	1	31	12.277	36.803	32.788	1.00	0.00
ATOM	251	N	HIS	1	32	10.865	39.200	32.331	1.00	0.00
ATOM	252	CA	HIS	1	32	9.972	40.079	31.653	1.00	0.00
ATOM	253	C	HIS	1	32	8.924	39.415	30.769	1.00	0.00
ATOM	254	O	HIS	1	32	9.202	38.493	30.018	1.00	0.00
ATOM	255	CB	HIS	1	32	10.760	41.083	30.810	1.00	0.00
ATOM	256	CG	HIS	1	32	10.498	42.477	31.288	1.00	0.00
ATOM	257	ND1	HIS	1	32	11.346	43.479	31.266	1.00	0.00
ATOM	258	CD2	HIS	1	32	9.246	43.049	31.602	1.00	0.00
ATOM	259	CE1	HIS	1	32	10.678	44.659	31.574	1.00	0.00
ATOM	260	NE2	HIS	1	32	9.377	44.389	31.784	1.00	0.00
ATOM	261	H	HIS	1	32	11.489	38.555	31.889	1.00	0.00
ATOM	262	1HD	HIS	1	32	12.295	43.246	31.197	1.00	0.00
ATOM	263	N	TRP	1	33	7.790	39.969	30.994	1.00	0.00
ATOM	264	CA	TRP	1	33	6.604	39.493	30.279	1.00	0.00
ATOM	265	C	TRP	1	33	6.205	40.551	29.240	1.00	0.00
ATOM	266	O	TRP	1	33	6.438	41.689	29.500	1.00	0.00
ATOM	267	CB	TRP	1	33	5.415	39.260	31.209	1.00	0.00
ATOM	268	CG	TRP	1	33	5.641	38.164	32.176	1.00	0.00
ATOM	269	CD1	TRP	1	33	6.812	37.983	32.936	1.00	0.00
ATOM	270	CD2	TRP	1	33	4.801	37.018	32.425	1.00	0.00
ATOM	271	NE1	TRP	1	33	6.752	36.776	33.576	1.00	0.00
ATOM	272	CE2	TRP	1	33	5.536	36.139	33.304	1.00	0.00
ATOM	273	CE3	TRP	1	33	3.526	36.671	31.930	1.00	0.00
ATOM	274	CZ2	TRP	1	33	5.043	34.854	33.676	1.00	0.00
ATOM	275	CZ3	TRP	1	33	3.036	35.429	32.346	1.00	0.00
ATOM	276	CH2	TRP	1	33	3.758	34.524	33.185	1.00	0.00
ATOM	277	H	TRP	1	33	7.826	40.663	31.713	1.00	0.00
ATOM	278	1HE	TRP	1	33	7.482	36.492	34.165	1.00	0.00
ATOM	279	N	GLN	1	34	5.696	40.048	28.134	1.00	0.00

Figure 1(con't)

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ATOM    280  CA  GLN 1   34       4.869  40.836  27.220  1.00  0.00
ATOM    281  C   GLN 1   34       3.424  40.408  27.177  1.00  0.00
ATOM    282  O   GLN 1   34       3.094  39.240  27.133  1.00  0.00
ATOM    283  CB  GLN 1   34       5.470  40.924  25.800  1.00  0.00
ATOM    284  CG  GLN 1   34       6.917  41.448  25.783  1.00  0.00
ATOM    285  CD  GLN 1   34       7.429  41.452  24.291  1.00  0.00
ATOM    286  OE1 GLN 1   34       7.612  42.380  23.559  1.00  0.00
ATOM    287  NE2 GLN 1   34       7.489  40.260  23.927  1.00  0.00
ATOM    288  H   GLN 1   34       5.517  39.064  28.146  1.00  0.00
ATOM    289 1HE2 GLN 1   34       7.323  39.442  24.478  1.00  0.00
ATOM    290 2HE2 GLN 1   34       7.792  40.263  22.974  1.00  0.00
ATOM    291  N   ALA 1   35       2.538  41.366  27.220  1.00  0.00
ATOM    292  CA  ALA 1   35       1.184  40.851  27.117  1.00  0.00
ATOM    293  C   ALA 1   35       0.289  41.720  26.273  1.00  0.00
ATOM    294  O   ALA 1   35       0.110  42.908  26.564  1.00  0.00
ATOM    295  CB  ALA 1   35       0.621  40.755  28.550  1.00  0.00
ATOM    296  H   ALA 1   35       2.893  42.286  27.389  1.00  0.00
ATOM    297  N   THR 1   36      -0.357  40.970  25.395  1.00  0.00
ATOM    298  CA  THR 1   36      -1.550  41.487  24.753  1.00  0.00
ATOM    299  C   THR 1   36      -2.696  41.829  25.712  1.00  0.00
ATOM    300  O   THR 1   36      -3.280  41.022  26.401  1.00  0.00
ATOM    301  CB  THR 1   36      -2.200  40.523  23.714  1.00  0.00
ATOM    302  OG1 THR 1   36      -1.176  39.765  22.985  1.00  0.00
ATOM    303  CG2 THR 1   36      -3.302  41.301  22.943  1.00  0.00
ATOM    304  H   THR 1   36       0.086  40.113  25.129  1.00  0.00
ATOM    305 1HG  THR 1   36      -1.335  40.089  22.109  1.00  0.00
ATOM    306  N   ILE 1   37      -3.026  43.130  25.648  1.00  0.00
ATOM    307  CA  ILE 1   37      -4.191  43.548  26.429  1.00  0.00
ATOM    308  C   ILE 1   37      -5.298  44.216  25.630  1.00  0.00
ATOM    309  O   ILE 1   37      -5.101  45.204  24.964  1.00  0.00
ATOM    310  CB  ILE 1   37      -3.797  44.351  27.724  1.00  0.00
ATOM    311  CG1 ILE 1   37      -4.897  45.181  28.449  1.00  0.00
ATOM    312  CG2 ILE 1   37      -2.542  45.130  27.448  1.00  0.00
ATOM    313  CD1 ILE 1   37      -4.556  46.013  29.659  1.00  0.00
ATOM    314  H   ILE 1   37      -2.472  43.740  25.081  1.00  0.00
ATOM    315  N   MET 1   38      -6.458  43.574  25.878  1.00  0.00
ATOM    316  CA  MET 1   38      -7.586  44.220  25.347  1.00  0.00
ATOM    317  C   MET 1   38      -8.605  44.872  26.322  1.00  0.00
ATOM    318  O   MET 1   38      -8.349  45.935  26.893  1.00  0.00
ATOM    319  CB  MET 1   38      -8.343  43.241  24.447  1.00  0.00
ATOM    320  CG  MET 1   38      -7.470  42.311  23.603  1.00  0.00
ATOM    321  SD  MET 1   38      -8.288  40.905  22.853  1.00  0.00
ATOM    322  CE  MET 1   38      -9.622  41.838  22.065  1.00  0.00
ATOM    323  H   MET 1   38      -6.505  42.757  26.452  1.00  0.00
ATOM    324  N   GLY 1   39      -9.770  44.272  26.496  1.00  0.00
ATOM    325  CA  GLY 1   39     -11.056  44.966  26.850  1.00  0.00
ATOM    326  C   GLY 1   39     -12.298  44.411  26.038  1.00  0.00
ATOM    327  O   GLY 1   39     -12.214  43.940  24.916  1.00  0.00
ATOM    328  H   GLY 1   39      -9.966  43.294  26.425  1.00  0.00
ATOM    329  N   PRO 1   40     -13.477  44.500  26.766  1.00  0.00
ATOM    330  CA  PRO 1   40     -14.704  43.852  26.332  1.00  0.00
ATOM    331  C   PRO 1   40     -15.431  44.406  25.096  1.00  0.00
ATOM    332  O   PRO 1   40     -15.378  45.605  24.835  1.00  0.00
ATOM    333  CB  PRO 1   40     -15.528  43.836  27.644  1.00  0.00
ATOM    334  CG  PRO 1   40     -15.102  45.100  28.414  1.00  0.00
ATOM    335  CD  PRO 1   40     -13.575  45.060  28.122  1.00  0.00
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Figure 1(con't)

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ATOM    336  N   ASN 1   41     -16.104  43.478  24.432  1.00  0.00
ATOM    337  CA  ASN 1   41     -16.866  43.806  23.227  1.00  0.00
ATOM    338  C   ASN 1   41     -17.788  45.030  23.243  1.00  0.00
ATOM    339  O   ASN 1   41     -18.334  45.404  24.266  1.00  0.00
ATOM    340  CB  ASN 1   41     -17.505  42.566  22.629  1.00  0.00
ATOM    341  CG  ASN 1   41     -17.457  42.783  21.100  1.00  0.00
ATOM    342  OD1 ASN 1   41     -16.424  42.515  20.518  1.00  0.00
ATOM    343  ND2 ASN 1   41     -18.580  43.205  20.495  1.00  0.00
ATOM    344  H   ASN 1   41     -16.031  42.509  24.671  1.00  0.00
ATOM    345 1HD2 ASN 1   41     -19.340  43.519  21.065  1.00  0.00
ATOM    346 2HD2 ASN 1   41     -18.839  43.307  19.534  1.00  0.00
ATOM    347  N   ASP 1   42     -17.706  45.666  22.075  1.00  0.00
ATOM    348  CA  ASP 1   42     -18.549  46.827  21.646  1.00  0.00
ATOM    349  C   ASP 1   42     -17.990  48.094  22.183  1.00  0.00
ATOM    350  O   ASP 1   42     -17.904  49.099  21.503  1.00  0.00
ATOM    351  CB  ASP 1   42     -20.049  46.643  22.001  1.00  0.00
ATOM    352  CG  ASP 1   42     -20.617  45.386  21.248  1.00  0.00
ATOM    353  OD1 ASP 1   42     -21.189  44.546  22.019  1.00  0.00
ATOM    354  OD2 ASP 1   42     -20.505  45.329  19.972  1.00  0.00
ATOM    355  H   ASP 1   42     -17.172  45.239  21.345  1.00  0.00
ATOM    356  N   SER 1   43     -17.518  47.956  23.425  1.00  0.00
ATOM    357  CA  SER 1   43     -16.981  49.076  24.283  1.00  0.00
ATOM    358  C   SER 1   43     -15.645  49.654  23.703  1.00  0.00
ATOM    359  O   SER 1   43     -14.885  49.017  22.898  1.00  0.00
ATOM    360  CB  SER 1   43     -16.864  48.550  25.721  1.00  0.00
ATOM    361  OG  SER 1   43     -17.907  47.578  25.969  1.00  0.00
ATOM    362  H   SER 1   43     -17.691  47.082  23.879  1.00  0.00
ATOM    363  HG  SER 1   43     -17.668  46.770  25.535  1.00  0.00
ATOM    364  N   PRO 1   44     -15.449  50.978  24.037  1.00  0.00
ATOM    365  CA  PRO 1   44     -14.337  51.686  23.444  1.00  0.00
ATOM    366  C   PRO 1   44     -12.965  51.042  23.266  1.00  0.00
ATOM    367  O   PRO 1   44     -12.323  50.986  22.187  1.00  0.00
ATOM    368  CB  PRO 1   44     -14.294  52.931  24.332  1.00  0.00
ATOM    369  CG  PRO 1   44     -15.749  53.253  24.642  1.00  0.00
ATOM    370  CD  PRO 1   44     -16.388  51.873  24.723  1.00  0.00
ATOM    371  N   TYR 1   45     -12.499  50.612  24.469  1.00  0.00
ATOM    372  CA  TYR 1   45     -11.173  49.936  24.432  1.00  0.00
ATOM    373  C   TYR 1   45     -10.989  48.618  23.768  1.00  0.00
ATOM    374  O   TYR 1   45      -9.874  48.082  23.625  1.00  0.00
ATOM    375  CB  TYR 1   45     -10.642  49.821  25.898  1.00  0.00
ATOM    376  CG  TYR 1   45     -10.263  51.093  26.551  1.00  0.00
ATOM    377  CD1 TYR 1   45     -11.055  51.437  27.637  1.00  0.00
ATOM    378  CD2 TYR 1   45      -9.186  51.866  26.062  1.00  0.00
ATOM    379  CE1 TYR 1   45     -10.678  52.632  28.338  1.00  0.00
ATOM    380  CE2 TYR 1   45      -8.954  53.120  26.707  1.00  0.00
ATOM    381  CZ  TYR 1   45      -9.696  53.503  27.827  1.00  0.00
ATOM    382  OH  TYR 1   45      -9.427  54.731  28.452  1.00  0.00
ATOM    383  H   TYR 1   45     -12.786  50.950  25.365  1.00  0.00
ATOM    384  HH  TYR 1   45      -9.015  55.269  27.788  1.00  0.00
ATOM    385  N   GLN 1   46     -12.094  48.046  23.382  1.00  0.00
ATOM    386  CA  GLN 1   46     -12.061  46.725  22.755  1.00  0.00
ATOM    387  C   GLN 1   46     -11.454  46.729  21.459  1.00  0.00
ATOM    388  O   GLN 1   46     -11.537  47.737  20.760  1.00  0.00
ATOM    389  CB  GLN 1   46     -13.469  46.126  22.604  1.00  0.00
ATOM    390  CG  GLN 1   46     -13.789  45.049  21.539  1.00  0.00
ATOM    391  CD  GLN 1   46     -14.461  45.627  20.354  1.00  0.00
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Figure 1(con't)

ATOM	392	OE1	GLN	1	46	-14.289	46.795	20.051	1.00	0.00
ATOM	393	NE2	GLN	1	46	-15.311	44.856	19.671	1.00	0.00
ATOM	394	H	GLN	1	46	-12.898	48.611	23.201	1.00	0.00
ATOM	395	1HE2	GLN	1	46	-15.436	43.884	19.867	1.00	0.00
ATOM	396	2HE2	GLN	1	46	-15.796	45.251	18.890	1.00	0.00
ATOM	397	N	GLY	1	47	-10.734	45.644	21.155	1.00	0.00
ATOM	398	CA	GLY	1	47	-10.114	45.605	19.848	1.00	0.00
ATOM	399	C	GLY	1	47	-8.629	45.843	19.905	1.00	0.00
ATOM	400	O	GLY	1	47	-7.769	45.119	19.319	1.00	0.00
ATOM	401	H	GLY	1	47	-10.775	44.822	21.723	1.00	0.00
ATOM	402	N	GLY	1	48	-8.271	46.947	20.695	1.00	0.00
ATOM	403	CA	GLY	1	48	-6.913	47.393	20.950	1.00	0.00
ATOM	404	C	GLY	1	48	-6.009	46.228	21.154	1.00	0.00
ATOM	405	O	GLY	1	48	-6.280	45.269	21.911	1.00	0.00
ATOM	406	H	GLY	1	48	-9.072	47.442	21.032	1.00	0.00
ATOM	407	N	VAL	1	49	-4.877	46.300	20.420	1.00	0.00
ATOM	408	CA	VAL	1	49	-3.846	45.346	20.774	1.00	0.00
ATOM	409	C	VAL	1	49	-2.700	46.129	21.429	1.00	0.00
ATOM	410	O	VAL	1	49	-1.856	46.847	20.841	1.00	0.00
ATOM	411	CB	VAL	1	49	-3.358	44.738	19.453	1.00	0.00
ATOM	412	CG1	VAL	1	49	-2.394	43.577	19.728	1.00	0.00
ATOM	413	CG2	VAL	1	49	-4.498	44.517	18.390	1.00	0.00
ATOM	414	H	VAL	1	49	-4.707	47.023	19.750	1.00	0.00
ATOM	415	N	PHE	1	50	-2.811	46.022	22.734	1.00	0.00
ATOM	416	CA	PHE	1	50	-1.793	46.690	23.383	1.00	0.00
ATOM	417	C	PHE	1	50	-0.835	45.766	23.937	1.00	0.00
ATOM	418	O	PHE	1	50	-1.082	44.564	24.001	1.00	0.00
ATOM	419	CB	PHE	1	50	-2.343	47.588	24.462	1.00	0.00
ATOM	420	CG	PHE	1	50	-3.767	48.162	24.266	1.00	0.00
ATOM	421	CD1	PHE	1	50	-4.158	48.819	23.058	1.00	0.00
ATOM	422	CD2	PHE	1	50	-4.648	48.064	25.365	1.00	0.00
ATOM	423	CE1	PHE	1	50	-5.442	49.326	22.959	1.00	0.00
ATOM	424	CE2	PHE	1	50	-5.989	48.477	25.179	1.00	0.00
ATOM	425	CZ	PHE	1	50	-6.378	49.138	23.978	1.00	0.00
ATOM	426	H	PHE	1	50	-3.535	45.534	23.221	1.00	0.00
ATOM	427	N	PHE	1	51	0.269	46.369	24.384	1.00	0.00
ATOM	428	CA	PHE	1	51	1.219	45.510	25.011	1.00	0.00
ATOM	429	C	PHE	1	51	1.628	46.101	26.372	1.00	0.00
ATOM	430	O	PHE	1	51	1.290	47.244	26.681	1.00	0.00
ATOM	431	CB	PHE	1	51	2.558	45.235	24.183	1.00	0.00
ATOM	432	CG	PHE	1	51	2.071	44.870	22.735	1.00	0.00
ATOM	433	CD1	PHE	1	51	1.474	43.648	22.482	1.00	0.00
ATOM	434	CD2	PHE	1	51	2.253	45.869	21.762	1.00	0.00
ATOM	435	CE1	PHE	1	51	1.003	43.443	21.104	1.00	0.00
ATOM	436	CE2	PHE	1	51	1.858	45.668	20.423	1.00	0.00
ATOM	437	CZ	PHE	1	51	1.236	44.497	20.130	1.00	0.00
ATOM	438	H	PHE	1	51	0.598	47.248	24.040	1.00	0.00
ATOM	439	N	LEU	1	52	2.130	45.091	27.132	1.00	0.00
ATOM	440	CA	LEU	1	52	2.325	45.227	28.576	1.00	0.00
ATOM	441	C	LEU	1	52	3.524	44.445	29.054	1.00	0.00
ATOM	442	O	LEU	1	52	3.530	43.203	29.019	1.00	0.00
ATOM	443	CB	LEU	1	52	1.065	44.789	29.287	1.00	0.00
ATOM	444	CG	LEU	1	52	0.938	45.233	30.789	1.00	0.00
ATOM	445	CD1	LEU	1	52	-0.220	46.185	30.933	1.00	0.00
ATOM	446	CD2	LEU	1	52	0.653	44.204	31.814	1.00	0.00
ATOM	447	H	LEU	1	52	2.068	44.177	26.732	1.00	0.00

Figure 1(con't)

ATOM	448	N	THR	1	53	4.567	45.174	29.416	1.00	0.00
ATOM	449	CA	THR	1	53	5.541	44.339	30.004	1.00	0.00
ATOM	450	C	THR	1	53	5.394	44.249	31.552	1.00	0.00
ATOM	451	O	THR	1	53	5.698	45.208	32.281	1.00	0.00
ATOM	452	CB	THR	1	53	6.993	44.839	29.721	1.00	0.00
ATOM	453	OG1	THR	1	53	7.141	46.178	30.117	1.00	0.00
ATOM	454	CG2	THR	1	53	7.449	44.539	28.336	1.00	0.00
ATOM	455	H	THR	1	53	4.610	46.165	29.290	1.00	0.00
ATOM	456	1HG	THR	1	53	6.693	46.593	29.392	1.00	0.00
ATOM	457	N	ILE	1	54	5.055	43.019	32.006	1.00	0.00
ATOM	458	CA	ILE	1	54	5.201	42.975	33.500	1.00	0.00
ATOM	459	C	ILE	1	54	6.483	42.187	33.824	1.00	0.00
ATOM	460	O	ILE	1	54	6.624	41.049	33.449	1.00	0.00
ATOM	461	CB	ILE	1	54	3.895	42.546	34.056	1.00	0.00
ATOM	462	CG1	ILE	1	54	4.116	42.239	35.538	1.00	0.00
ATOM	463	CG2	ILE	1	54	3.293	41.330	33.449	1.00	0.00
ATOM	464	CD1	ILE	1	54	2.835	42.116	36.297	1.00	0.00
ATOM	465	H	ILE	1	54	4.883	42.200	31.459	1.00	0.00
ATOM	466	N	HIS	1	55	7.356	42.905	34.533	1.00	0.00
ATOM	467	CA	HIS	1	55	8.680	42.432	35.034	1.00	0.00
ATOM	468	C	HIS	1	55	8.488	41.851	36.430	1.00	0.00
ATOM	469	O	HIS	1	55	8.711	42.401	37.499	1.00	0.00
ATOM	470	CB	HIS	1	55	9.677	43.626	35.221	1.00	0.00
ATOM	471	CG	HIS	1	55	11.084	43.145	35.610	1.00	0.00
ATOM	472	ND1	HIS	1	55	11.463	42.849	36.889	1.00	0.00
ATOM	473	CD2	HIS	1	55	12.160	43.008	34.734	1.00	0.00
ATOM	474	CE1	HIS	1	55	12.798	42.553	36.874	1.00	0.00
ATOM	475	NE2	HIS	1	55	13.166	42.652	35.589	1.00	0.00
ATOM	476	H	HIS	1	55	6.985	43.825	34.656	1.00	0.00
ATOM	477	1HD	HIS	1	55	10.779	42.792	37.588	1.00	0.00
ATOM	478	N	PHE	1	56	8.004	40.579	36.294	1.00	0.00
ATOM	479	CA	PHE	1	56	8.124	39.740	37.478	1.00	0.00
ATOM	480	C	PHE	1	56	9.564	39.404	37.759	1.00	0.00
ATOM	481	O	PHE	1	56	10.111	38.735	36.928	1.00	0.00
ATOM	482	CB	PHE	1	56	7.431	38.414	37.221	1.00	0.00
ATOM	483	CG	PHE	1	56	5.957	38.636	37.218	1.00	0.00
ATOM	484	CD1	PHE	1	56	5.243	38.642	38.488	1.00	0.00
ATOM	485	CD2	PHE	1	56	5.258	38.651	36.021	1.00	0.00
ATOM	486	CE1	PHE	1	56	3.843	38.681	38.472	1.00	0.00
ATOM	487	CE2	PHE	1	56	3.883	38.677	36.013	1.00	0.00
ATOM	488	CZ	PHE	1	56	3.180	38.671	37.227	1.00	0.00
ATOM	489	H	PHE	1	56	8.146	40.122	35.416	1.00	0.00
ATOM	490	N	PRO	1	57	10.161	40.000	38.828	1.00	0.00
ATOM	491	CA	PRO	1	57	11.669	39.843	38.911	1.00	0.00
ATOM	492	C	PRO	1	57	12.092	38.428	39.104	1.00	0.00
ATOM	493	O	PRO	1	57	11.362	37.470	39.343	1.00	0.00
ATOM	494	CB	PRO	1	57	12.003	40.789	40.050	1.00	0.00
ATOM	495	CG	PRO	1	57	10.739	40.883	40.945	1.00	0.00
ATOM	496	CD	PRO	1	57	9.576	40.703	39.952	1.00	0.00
ATOM	497	N	THR	1	58	13.424	38.247	38.912	1.00	0.00
ATOM	498	CA	THR	1	58	14.071	37.056	39.470	1.00	0.00
ATOM	499	C	THR	1	58	13.788	36.737	40.841	1.00	0.00
ATOM	500	O	THR	1	58	13.926	35.629	41.294	1.00	0.00
ATOM	501	CB	THR	1	58	15.541	37.145	39.032	1.00	0.00
ATOM	502	OG1	THR	1	58	15.680	37.609	37.672	1.00	0.00
ATOM	503	CG2	THR	1	58	16.131	35.762	39.182	1.00	0.00

Figure 1(con't)

ATOM	504	H	THR	1	58	14.036	38.966	38.583	1.00	0.00
ATOM	505	1HG	THR	1	58	16.524	37.297	37.373	1.00	0.00
ATOM	506	N	ASP	1	59	13.457	37.777	41.583	1.00	0.00
ATOM	507	CA	ASP	1	59	13.181	37.664	43.011	1.00	0.00
ATOM	508	C	ASP	1	59	11.769	37.504	43.490	1.00	0.00
ATOM	509	O	ASP	1	59	11.159	38.230	44.245	1.00	0.00
ATOM	510	CB	ASP	1	59	13.889	38.750	43.734	1.00	0.00
ATOM	511	CG	ASP	1	59	13.491	40.164	43.290	1.00	0.00
ATOM	512	OD1	ASP	1	59	14.211	40.777	42.414	1.00	0.00
ATOM	513	OD2	ASP	1	59	12.597	40.779	43.786	1.00	0.00
ATOM	514	H	ASP	1	59	13.329	38.682	41.178	1.00	0.00
ATOM	515	N	TYR	1	60	11.264	36.412	43.011	1.00	0.00
ATOM	516	CA	TYR	1	60	9.821	36.218	43.226	1.00	0.00
ATOM	517	C	TYR	1	60	9.406	35.407	44.477	1.00	0.00
ATOM	518	O	TYR	1	60	10.033	34.441	44.781	1.00	0.00
ATOM	519	CB	TYR	1	60	9.157	35.843	41.829	1.00	0.00
ATOM	520	CG	TYR	1	60	7.838	36.612	41.789	1.00	0.00
ATOM	521	CD1	TYR	1	60	8.034	37.990	41.682	1.00	0.00
ATOM	522	CD2	TYR	1	60	6.546	36.030	41.874	1.00	0.00
ATOM	523	CE1	TYR	1	60	6.972	38.870	41.721	1.00	0.00
ATOM	524	CE2	TYR	1	60	5.438	36.950	41.740	1.00	0.00
ATOM	525	CZ	TYR	1	60	5.729	38.357	41.751	1.00	0.00
ATOM	526	OH	TYR	1	60	4.710	39.254	41.968	1.00	0.00
ATOM	527	H	TYR	1	60	11.803	35.930	42.321	1.00	0.00
ATOM	528	HH	TYR	1	60	4.929	39.846	42.676	1.00	0.00
ATOM	529	N	PRO	1	61	8.341	35.745	45.277	1.00	0.00
ATOM	530	CA	PRO	1	61	7.611	36.986	45.163	1.00	0.00
ATOM	531	C	PRO	1	61	8.031	38.127	46.103	1.00	0.00
ATOM	532	O	PRO	1	61	7.544	38.281	47.197	1.00	0.00
ATOM	533	CB	PRO	1	61	6.241	36.440	45.549	1.00	0.00
ATOM	534	CG	PRO	1	61	6.451	35.361	46.551	1.00	0.00
ATOM	535	CD	PRO	1	61	7.874	34.846	46.340	1.00	0.00
ATOM	536	N	PHE	1	62	8.921	39.015	45.665	1.00	0.00
ATOM	537	CA	PHE	1	62	9.316	39.953	46.675	1.00	0.00
ATOM	538	C	PHE	1	62	9.091	41.436	46.494	1.00	0.00
ATOM	539	O	PHE	1	62	8.277	42.242	47.033	1.00	0.00
ATOM	540	CB	PHE	1	62	10.835	39.726	47.093	1.00	0.00
ATOM	541	CG	PHE	1	62	11.170	38.343	47.627	1.00	0.00
ATOM	542	CD1	PHE	1	62	10.256	37.516	48.364	1.00	0.00
ATOM	543	CD2	PHE	1	62	12.483	37.929	47.366	1.00	0.00
ATOM	544	CE1	PHE	1	62	10.701	36.264	48.835	1.00	0.00
ATOM	545	CE2	PHE	1	62	12.959	36.670	47.863	1.00	0.00
ATOM	546	CZ	PHE	1	62	12.047	35.848	48.625	1.00	0.00
ATOM	547	H	PHE	1	62	9.595	38.814	44.954	1.00	0.00
ATOM	548	N	LYS	1	63	9.863	41.843	45.495	1.00	0.00
ATOM	549	CA	LYS	1	63	9.548	43.072	44.849	1.00	0.00
ATOM	550	C	LYS	1	63	8.397	43.143	43.796	1.00	0.00
ATOM	551	O	LYS	1	63	8.195	42.199	42.989	1.00	0.00
ATOM	552	CB	LYS	1	63	10.812	43.763	44.268	1.00	0.00
ATOM	553	CG	LYS	1	63	11.675	44.228	45.486	1.00	0.00
ATOM	554	CD	LYS	1	63	13.008	44.744	45.085	1.00	0.00
ATOM	555	CE	LYS	1	63	14.141	43.689	44.873	1.00	0.00
ATOM	556	NZ	LYS	1	63	13.885	43.084	43.628	1.00	0.00
ATOM	557	H	LYS	1	63	10.564	41.264	45.080	1.00	0.00
ATOM	558	1HZ	LYS	1	63	13.607	43.721	42.854	1.00	0.00
ATOM	559	2HZ	LYS	1	63	14.604	42.424	43.268	1.00	0.00

Figure 1(con't)

ATOM	560	3HZ	LYS	1	63	13.094	42.434	43.815	1.00	0.00
ATOM	561	N	PRO	1	64	7.612	44.296	44.014	1.00	0.00
ATOM	562	CA	PRO	1	64	6.552	44.555	43.047	1.00	0.00
ATOM	563	C	PRO	1	64	7.019	44.767	41.595	1.00	0.00
ATOM	564	O	PRO	1	64	7.827	45.556	41.196	1.00	0.00
ATOM	565	CB	PRO	1	64	5.886	45.784	43.752	1.00	0.00
ATOM	566	CG	PRO	1	64	6.176	45.623	45.213	1.00	0.00
ATOM	567	CD	PRO	1	64	7.675	45.291	45.131	1.00	0.00
ATOM	568	N	PRO	1	65	6.468	43.847	40.815	1.00	0.00
ATOM	569	CA	PRO	1	65	6.866	43.890	39.421	1.00	0.00
ATOM	570	C	PRO	1	65	6.657	45.256	38.732	1.00	0.00
ATOM	571	O	PRO	1	65	5.727	46.018	38.928	1.00	0.00
ATOM	572	CB	PRO	1	65	6.066	42.674	38.836	1.00	0.00
ATOM	573	CG	PRO	1	65	5.450	41.854	39.988	1.00	0.00
ATOM	574	CD	PRO	1	65	5.640	42.744	41.175	1.00	0.00
ATOM	575	N	LYS	1	66	7.616	45.558	37.920	1.00	0.00
ATOM	576	CA	LYS	1	66	7.582	46.638	36.943	1.00	0.00
ATOM	577	C	LYS	1	66	6.677	46.420	35.758	1.00	0.00
ATOM	578	O	LYS	1	66	6.975	45.573	34.895	1.00	0.00
ATOM	579	CB	LYS	1	66	9.042	47.057	36.632	1.00	0.00
ATOM	580	CG	LYS	1	66	9.026	47.916	35.359	1.00	0.00
ATOM	581	CD	LYS	1	66	9.426	47.170	34.096	1.00	0.00
ATOM	582	CE	LYS	1	66	8.561	47.715	32.960	1.00	0.00
ATOM	583	NZ	LYS	1	66	7.593	46.650	32.604	1.00	0.00
ATOM	584	H	LYS	1	66	8.315	44.850	37.823	1.00	0.00
ATOM	585	1HZ	LYS	1	66	7.202	46.096	33.393	1.00	0.00
ATOM	586	2HZ	LYS	1	66	6.840	46.784	31.900	1.00	0.00
ATOM	587	3HZ	LYS	1	66	8.051	45.940	31.997	1.00	0.00
ATOM	588	N	VAL	1	67	5.641	47.237	35.914	1.00	0.00
ATOM	589	CA	VAL	1	67	4.618	47.092	34.890	1.00	0.00
ATOM	590	C	VAL	1	67	4.669	48.202	33.838	1.00	0.00
ATOM	591	O	VAL	1	67	5.038	49.290	34.212	1.00	0.00
ATOM	592	CB	VAL	1	67	3.210	47.149	35.616	1.00	0.00
ATOM	593	CG1	VAL	1	67	2.008	47.020	34.713	1.00	0.00
ATOM	594	CG2	VAL	1	67	3.138	46.027	36.596	1.00	0.00
ATOM	595	H	VAL	1	67	5.652	47.816	36.730	1.00	0.00
ATOM	596	N	ALA	1	68	4.284	47.890	32.576	1.00	0.00
ATOM	597	CA	ALA	1	68	4.063	49.030	31.594	1.00	0.00
ATOM	598	C	ALA	1	68	3.210	48.782	30.295	1.00	0.00
ATOM	599	O	ALA	1	68	3.050	47.648	29.844	1.00	0.00
ATOM	600	CB	ALA	1	68	5.339	49.726	31.204	1.00	0.00
ATOM	601	H	ALA	1	68	3.936	46.964	32.435	1.00	0.00
ATOM	602	N	PHE	1	69	2.744	49.948	29.729	1.00	0.00
ATOM	603	CA	PHE	1	69	2.170	49.817	28.428	1.00	0.00
ATOM	604	C	PHE	1	69	3.003	49.993	27.243	1.00	0.00
ATOM	605	O	PHE	1	69	4.174	50.197	27.488	1.00	0.00
ATOM	606	CB	PHE	1	69	1.005	50.861	28.439	1.00	0.00
ATOM	607	CG	PHE	1	69	-0.236	50.170	29.024	1.00	0.00
ATOM	608	CD1	PHE	1	69	-0.571	50.303	30.370	1.00	0.00
ATOM	609	CD2	PHE	1	69	-1.184	49.627	28.119	1.00	0.00
ATOM	610	CE1	PHE	1	69	-1.950	49.879	30.749	1.00	0.00
ATOM	611	CE2	PHE	1	69	-2.510	49.317	28.496	1.00	0.00
ATOM	612	CZ	PHE	1	69	-2.919	49.553	29.836	1.00	0.00
ATOM	613	H	PHE	1	69	3.122	50.795	30.100	1.00	0.00
ATOM	614	N	THR	1	70	2.418	49.796	26.051	1.00	0.00
ATOM	615	CA	THR	1	70	3.174	50.059	24.865	1.00	0.00

Figure 1(con't)

ATOM	616	C	THR	1	70	2.540	50.869	23.691	1.00	0.00
ATOM	617	O	THR	1	70	3.101	51.454	22.774	1.00	0.00
ATOM	618	CB	THR	1	70	3.823	48.693	24.425	1.00	0.00
ATOM	619	OG1	THR	1	70	4.392	47.934	25.445	1.00	0.00
ATOM	620	CG2	THR	1	70	5.058	48.811	23.431	1.00	0.00
ATOM	621	H	THR	1	70	1.520	49.357	26.083	1.00	0.00
ATOM	622	1HG	THR	1	70	4.658	48.583	26.082	1.00	0.00
ATOM	623	N	THR	1	71	1.197	50.942	23.754	1.00	0.00
ATOM	624	CA	THR	1	71	0.474	51.874	22.977	1.00	0.00
ATOM	625	C	THR	1	71	0.307	53.101	23.855	1.00	0.00
ATOM	626	O	THR	1	71	0.482	52.993	25.082	1.00	0.00
ATOM	627	CB	THR	1	71	-0.890	51.230	22.586	1.00	0.00
ATOM	628	OG1	THR	1	71	-1.547	51.870	21.495	1.00	0.00
ATOM	629	CG2	THR	1	71	-1.785	51.219	23.771	1.00	0.00
ATOM	630	H	THR	1	71	0.626	50.488	24.439	1.00	0.00
ATOM	631	1HG	THR	1	71	-2.411	51.480	21.469	1.00	0.00
ATOM	632	N	ARG	1	72	-0.235	54.173	23.226	1.00	0.00
ATOM	633	CA	ARG	1	72	-0.698	55.208	24.180	1.00	0.00
ATOM	634	C	ARG	1	72	-2.115	55.840	23.974	1.00	0.00
ATOM	635	O	ARG	1	72	-2.217	57.065	23.776	1.00	0.00
ATOM	636	CB	ARG	1	72	0.288	56.308	24.307	1.00	0.00
ATOM	637	CG	ARG	1	72	0.826	56.516	25.720	1.00	0.00
ATOM	638	CD	ARG	1	72	-0.223	57.282	26.573	1.00	0.00
ATOM	639	NE	ARG	1	72	-0.810	58.398	25.780	1.00	0.00
ATOM	640	CZ	ARG	1	72	-1.820	59.012	26.451	1.00	0.00
ATOM	641	NH1	ARG	1	72	-2.145	58.515	27.586	1.00	0.00
ATOM	642	NH2	ARG	1	72	-2.355	60.127	25.927	1.00	0.00
ATOM	643	H	ARG	1	72	-0.234	54.315	22.236	1.00	0.00
ATOM	644	HE	ARG	1	72	-0.329	58.774	24.988	1.00	0.00
ATOM	645	1HH1	ARG	1	72	-2.785	59.051	28.137	1.00	0.00
ATOM	646	2HH1	ARG	1	72	-1.825	57.675	28.024	1.00	0.00
ATOM	647	1HH2	ARG	1	72	-3.097	60.500	26.484	1.00	0.00
ATOM	648	2HH2	ARG	1	72	-2.152	60.596	25.068	1.00	0.00
ATOM	649	N	ILE	1	73	-3.075	54.932	24.098	1.00	0.00
ATOM	650	CA	ILE	1	73	-4.455	55.301	23.856	1.00	0.00
ATOM	651	C	ILE	1	73	-5.133	55.989	25.011	1.00	0.00
ATOM	652	O	ILE	1	73	-5.141	55.445	26.100	1.00	0.00
ATOM	653	CB	ILE	1	73	-5.320	54.019	23.424	1.00	0.00
ATOM	654	CG1	ILE	1	73	-6.850	54.247	23.209	1.00	0.00
ATOM	655	CG2	ILE	1	73	-5.101	52.911	24.470	1.00	0.00
ATOM	656	CD1	ILE	1	73	-7.640	52.943	22.791	1.00	0.00
ATOM	657	H	ILE	1	73	-2.810	53.985	24.276	1.00	0.00
ATOM	658	N	TYR	1	74	-5.586	57.222	24.931	1.00	0.00
ATOM	659	CA	TYR	1	74	-6.264	58.008	25.978	1.00	0.00
ATOM	660	C	TYR	1	74	-6.963	57.448	27.192	1.00	0.00
ATOM	661	O	TYR	1	74	-8.075	56.932	27.127	1.00	0.00
ATOM	662	CB	TYR	1	74	-7.256	58.973	25.383	1.00	0.00
ATOM	663	CG	TYR	1	74	-6.545	60.286	24.901	1.00	0.00
ATOM	664	CD1	TYR	1	74	-6.956	61.516	25.449	1.00	0.00
ATOM	665	CD2	TYR	1	74	-5.569	60.181	23.917	1.00	0.00
ATOM	666	CE1	TYR	1	74	-6.330	62.685	25.001	1.00	0.00
ATOM	667	CE2	TYR	1	74	-4.903	61.360	23.491	1.00	0.00
ATOM	668	CZ	TYR	1	74	-5.267	62.542	24.077	1.00	0.00
ATOM	669	OH	TYR	1	74	-4.459	63.643	23.767	1.00	0.00
ATOM	670	H	TYR	1	74	-5.424	57.697	24.066	1.00	0.00
ATOM	671	HH	TYR	1	74	-3.605	63.327	23.505	1.00	0.00

Figure 1(con't)

ATOM	672	N	HIS	1	75	-6.244	57.542	28.315	1.00	0.00
ATOM	673	CA	HIS	1	75	-6.712	57.415	29.691	1.00	0.00
ATOM	674	C	HIS	1	75	-5.809	58.147	30.656	1.00	0.00
ATOM	675	O	HIS	1	75	-4.618	58.037	30.567	1.00	0.00
ATOM	676	CB	HIS	1	75	-6.903	55.932	30.164	1.00	0.00
ATOM	677	CG	HIS	1	75	-7.735	55.806	31.446	1.00	0.00
ATOM	678	ND1	HIS	1	75	-7.320	55.110	32.508	1.00	0.00
ATOM	679	CD2	HIS	1	75	-9.064	56.208	31.661	1.00	0.00
ATOM	680	CE1	HIS	1	75	-8.337	55.061	33.430	1.00	0.00
ATOM	681	NE2	HIS	1	75	-9.429	55.714	32.910	1.00	0.00
ATOM	682	H	HIS	1	75	-5.350	57.933	28.095	1.00	0.00
ATOM	683	1HD	HIS	1	75	-6.505	54.575	32.609	1.00	0.00
ATOM	684	N	PRO	1	76	-6.406	58.853	31.622	1.00	0.00
ATOM	685	CA	PRO	1	76	-5.631	59.218	32.828	1.00	0.00
ATOM	686	C	PRO	1	76	-4.689	58.242	33.509	1.00	0.00
ATOM	687	O	PRO	1	76	-3.545	58.615	33.836	1.00	0.00
ATOM	688	CB	PRO	1	76	-6.733	59.744	33.703	1.00	0.00
ATOM	689	CG	PRO	1	76	-8.079	59.421	33.110	1.00	0.00
ATOM	690	CD	PRO	1	76	-7.793	59.273	31.629	1.00	0.00
ATOM	691	N	ASN	1	77	-5.120	56.969	33.592	1.00	0.00
ATOM	692	CA	ASN	1	77	-4.149	55.995	34.023	1.00	0.00
ATOM	693	C	ASN	1	77	-3.232	55.350	32.975	1.00	0.00
ATOM	694	O	ASN	1	77	-2.235	54.686	33.293	1.00	0.00
ATOM	695	CB	ASN	1	77	-4.544	55.069	35.221	1.00	0.00
ATOM	696	CG	ASN	1	77	-5.398	53.859	34.799	1.00	0.00
ATOM	697	OD1	ASN	1	77	-5.269	53.390	33.660	1.00	0.00
ATOM	698	ND2	ASN	1	77	-6.264	53.533	35.724	1.00	0.00
ATOM	699	H	ASN	1	77	-6.008	56.604	33.313	1.00	0.00
ATOM	700	1HD2	ASN	1	77	-6.190	53.971	36.620	1.00	0.00
ATOM	701	2HD2	ASN	1	77	-6.951	52.815	35.616	1.00	0.00
ATOM	702	N	ILE	1	78	-3.577	55.500	31.719	1.00	0.00
ATOM	703	CA	ILE	1	78	-2.428	55.111	30.819	1.00	0.00
ATOM	704	C	ILE	1	78	-1.366	56.277	30.720	1.00	0.00
ATOM	705	O	ILE	1	78	-1.137	56.911	29.708	1.00	0.00
ATOM	706	CB	ILE	1	78	-2.914	54.640	29.485	1.00	0.00
ATOM	707	CG1	ILE	1	78	-4.001	53.586	29.802	1.00	0.00
ATOM	708	CG2	ILE	1	78	-1.718	53.970	28.701	1.00	0.00
ATOM	709	CD1	ILE	1	78	-4.663	53.021	28.578	1.00	0.00
ATOM	710	H	ILE	1	78	-4.240	56.191	31.434	1.00	0.00
ATOM	711	N	ASN	1	79	-0.702	56.476	31.895	1.00	0.00
ATOM	712	CA	ASN	1	79	0.362	57.504	31.918	1.00	0.00
ATOM	713	C	ASN	1	79	1.462	57.177	30.980	1.00	0.00
ATOM	714	O	ASN	1	79	1.783	56.010	30.852	1.00	0.00
ATOM	715	CB	ASN	1	79	0.977	57.697	33.357	1.00	0.00
ATOM	716	CG	ASN	1	79	1.977	58.941	33.383	1.00	0.00
ATOM	717	OD1	ASN	1	79	3.102	58.857	32.913	1.00	0.00
ATOM	718	ND2	ASN	1	79	1.421	59.936	34.047	1.00	0.00
ATOM	719	H	ASN	1	79	-0.879	55.970	32.740	1.00	0.00
ATOM	720	1HD2	ASN	1	79	0.480	59.871	34.380	1.00	0.00
ATOM	721	2HD2	ASN	1	79	1.919	60.793	34.181	1.00	0.00
ATOM	722	N	SER	1	80	2.012	58.274	30.296	1.00	0.00
ATOM	723	CA	SER	1	80	3.020	58.037	29.307	1.00	0.00
ATOM	724	C	SER	1	80	4.213	57.172	29.722	1.00	0.00
ATOM	725	O	SER	1	80	4.736	56.463	28.906	1.00	0.00
ATOM	726	CB	SER	1	80	3.540	59.374	28.740	1.00	0.00
ATOM	727	OG	SER	1	80	2.464	60.229	28.410	1.00	0.00

Figure 1(con't)

ATOM	728	H	SER	1	80	1.733	59.222	30.444	1.00	0.00
ATOM	729	HG	SER	1	80	2.142	59.977	27.555	1.00	0.00
ATOM	730	N	ASN	1	81	4.499	57.059	31.048	1.00	0.00
ATOM	731	CA	ASN	1	81	5.499	56.121	31.571	1.00	0.00
ATOM	732	C	ASN	1	81	5.049	54.722	31.893	1.00	0.00
ATOM	733	O	ASN	1	81	5.800	53.806	32.205	1.00	0.00
ATOM	734	CB	ASN	1	81	6.239	56.638	32.776	1.00	0.00
ATOM	735	CG	ASN	1	81	5.190	57.043	33.835	1.00	0.00
ATOM	736	OD1	ASN	1	81	4.206	56.324	33.995	1.00	0.00
ATOM	737	ND2	ASN	1	81	5.364	58.167	34.505	1.00	0.00
ATOM	738	H	ASN	1	81	4.021	57.645	31.702	1.00	0.00
ATOM	739	1HD2	ASN	1	81	6.256	58.616	34.550	1.00	0.00
ATOM	740	2HD2	ASN	1	81	4.596	58.637	34.941	1.00	0.00
ATOM	741	N	GLY	1	82	3.733	54.599	31.889	1.00	0.00
ATOM	742	CA	GLY	1	82	3.169	53.260	32.012	1.00	0.00
ATOM	743	C	GLY	1	82	2.883	52.770	33.467	1.00	0.00
ATOM	744	O	GLY	1	82	2.757	51.537	33.677	1.00	0.00
ATOM	745	H	GLY	1	82	3.081	55.355	31.943	1.00	0.00
ATOM	746	N	SER	1	83	2.699	53.686	34.408	1.00	0.00
ATOM	747	CA	SER	1	83	2.182	53.325	35.707	1.00	0.00
ATOM	748	C	SER	1	83	0.653	53.291	35.565	1.00	0.00
ATOM	749	O	SER	1	83	0.005	53.943	34.723	1.00	0.00
ATOM	750	CB	SER	1	83	2.747	54.306	36.709	1.00	0.00
ATOM	751	OG	SER	1	83	4.143	54.436	36.565	1.00	0.00
ATOM	752	H	SER	1	83	2.728	54.661	34.188	1.00	0.00
ATOM	753	HG	SER	1	83	4.292	55.334	36.830	1.00	0.00
ATOM	754	N	ILE	1	84	0.097	52.428	36.385	1.00	0.00
ATOM	755	CA	ILE	1	84	-1.370	52.476	36.461	1.00	0.00
ATOM	756	C	ILE	1	84	-1.850	52.509	37.900	1.00	0.00
ATOM	757	O	ILE	1	84	-1.165	51.998	38.770	1.00	0.00
ATOM	758	CB	ILE	1	84	-1.937	51.310	35.649	1.00	0.00
ATOM	759	CG1	ILE	1	84	-0.929	50.116	35.676	1.00	0.00
ATOM	760	CG2	ILE	1	84	-2.392	51.652	34.199	1.00	0.00
ATOM	761	CD1	ILE	1	84	-0.862	49.238	36.911	1.00	0.00
ATOM	762	H	ILE	1	84	0.585	51.890	37.073	1.00	0.00
ATOM	763	N	CYS	1	85	-3.050	53.104	38.044	1.00	0.00
ATOM	764	CA	CYS	1	85	-3.456	53.377	39.430	1.00	0.00
ATOM	765	C	CYS	1	85	-3.946	52.219	40.300	1.00	0.00
ATOM	766	O	CYS	1	85	-3.154	51.631	40.977	1.00	0.00
ATOM	767	CB	CYS	1	85	-4.494	54.530	39.493	1.00	0.00
ATOM	768	SG	CYS	1	85	-3.719	56.051	38.899	1.00	0.00
ATOM	769	H	CYS	1	85	-3.555	53.567	37.316	1.00	0.00
ATOM	770	N	LEU	1	86	-5.235	51.872	40.178	1.00	0.00
ATOM	771	CA	LEU	1	86	-5.836	50.570	40.669	1.00	0.00
ATOM	772	C	LEU	1	86	-5.198	49.716	41.738	1.00	0.00
ATOM	773	O	LEU	1	86	-4.347	48.854	41.497	1.00	0.00
ATOM	774	CB	LEU	1	86	-6.178	49.687	39.435	1.00	0.00
ATOM	775	CG	LEU	1	86	-5.062	49.502	38.390	1.00	0.00
ATOM	776	CD1	LEU	1	86	-4.529	48.072	38.326	1.00	0.00
ATOM	777	CD2	LEU	1	86	-5.429	49.889	36.984	1.00	0.00
ATOM	778	H	LEU	1	86	-5.624	52.275	39.349	1.00	0.00
ATOM	779	N	ASP	1	87	-5.646	49.975	42.971	1.00	0.00
ATOM	780	CA	ASP	1	87	-5.525	49.028	44.088	1.00	0.00
ATOM	781	C	ASP	1	87	-4.109	48.504	44.263	1.00	0.00
ATOM	782	O	ASP	1	87	-3.363	49.082	45.066	1.00	0.00
ATOM	783	CB	ASP	1	87	-6.527	47.893	43.964	1.00	0.00

Figure 1(con't)

ATOM	784	CG	ASP	1	87	-6.431	46.788	45.001	1.00	0.00
ATOM	785	OD1	ASP	1	87	-6.114	47.067	46.154	1.00	0.00
ATOM	786	OD2	ASP	1	87	-6.744	45.628	44.680	1.00	0.00
ATOM	787	H	ASP	1	87	-6.293	50.722	43.123	1.00	0.00
ATOM	788	N	ILE	1	88	-3.811	47.376	43.540	1.00	0.00
ATOM	789	CA	ILE	1	88	-2.601	46.573	43.737	1.00	0.00
ATOM	790	C	ILE	1	88	-1.296	47.330	43.558	1.00	0.00
ATOM	791	O	ILE	1	88	-0.504	47.300	44.477	1.00	0.00
ATOM	792	CB	ILE	1	88	-2.715	45.322	42.836	1.00	0.00
ATOM	793	CG1	ILE	1	88	-2.555	45.432	41.275	1.00	0.00
ATOM	794	CG2	ILE	1	88	-4.113	44.647	42.978	1.00	0.00
ATOM	795	CD1	ILE	1	88	-2.522	44.051	40.547	1.00	0.00
ATOM	796	H	ILE	1	88	-4.311	47.348	42.674	1.00	0.00
ATOM	797	N	LEU	1	89	-1.124	48.012	42.405	1.00	0.00
ATOM	798	CA	LEU	1	89	-0.037	48.937	42.290	1.00	0.00
ATOM	799	C	LEU	1	89	-0.284	50.287	42.862	1.00	0.00
ATOM	800	O	LEU	1	89	-0.472	51.269	42.113	1.00	0.00
ATOM	801	CB	LEU	1	89	0.443	49.094	40.838	1.00	0.00
ATOM	802	CG	LEU	1	89	1.420	48.043	40.288	1.00	0.00
ATOM	803	CD1	LEU	1	89	2.636	47.915	41.237	1.00	0.00
ATOM	804	CD2	LEU	1	89	0.675	46.722	39.962	1.00	0.00
ATOM	805	H	LEU	1	89	-1.933	48.260	41.873	1.00	0.00
ATOM	806	N	ARG	1	90	-0.418	50.340	44.189	1.00	0.00
ATOM	807	CA	ARG	1	90	-0.026	51.384	45.135	1.00	0.00
ATOM	808	C	ARG	1	90	-0.473	51.119	46.614	1.00	0.00
ATOM	809	O	ARG	1	90	0.338	50.878	47.480	1.00	0.00
ATOM	810	CB	ARG	1	90	-0.202	52.892	44.694	1.00	0.00
ATOM	811	CG	ARG	1	90	-1.614	53.327	44.386	1.00	0.00
ATOM	812	CD	ARG	1	90	-1.771	54.741	43.914	1.00	0.00
ATOM	813	NE	ARG	1	90	-3.140	55.176	43.940	1.00	0.00
ATOM	814	CZ	ARG	1	90	-3.469	56.121	43.129	1.00	0.00
ATOM	815	NH1	ARG	1	90	-4.669	56.743	43.266	1.00	0.00
ATOM	816	NH2	ARG	1	90	-2.772	56.487	42.010	1.00	0.00
ATOM	817	H	ARG	1	90	-0.600	49.477	44.659	1.00	0.00
ATOM	818	HE	ARG	1	90	-3.649	54.776	44.702	1.00	0.00
ATOM	819	1HH1	ARG	1	90	-4.832	57.565	42.721	1.00	0.00
ATOM	820	2HH1	ARG	1	90	-5.240	56.526	44.058	1.00	0.00
ATOM	821	1HH2	ARG	1	90	-3.123	57.247	41.464	1.00	0.00
ATOM	822	2HH2	ARG	1	90	-1.861	56.172	41.743	1.00	0.00
ATOM	823	N	SER	1	91	-1.779	51.132	46.880	1.00	0.00
ATOM	824	CA	SER	1	91	-2.246	50.840	48.231	1.00	0.00
ATOM	825	C	SER	1	91	-2.039	49.496	48.865	1.00	0.00
ATOM	826	O	SER	1	91	-2.155	49.290	50.084	1.00	0.00
ATOM	827	CB	SER	1	91	-3.706	51.221	48.212	1.00	0.00
ATOM	828	OG	SER	1	91	-3.945	52.494	47.464	1.00	0.00
ATOM	829	H	SER	1	91	-2.454	51.157	46.142	1.00	0.00
ATOM	830	HG	SER	1	91	-4.217	53.128	48.114	1.00	0.00
ATOM	831	N	GLN	1	92	-1.695	48.524	47.995	1.00	0.00
ATOM	832	CA	GLN	1	92	-1.634	47.185	48.509	1.00	0.00
ATOM	833	C	GLN	1	92	-0.236	46.696	48.873	1.00	0.00
ATOM	834	O	GLN	1	92	0.410	46.150	47.994	1.00	0.00
ATOM	835	CB	GLN	1	92	-2.345	46.228	47.634	1.00	0.00
ATOM	836	CG	GLN	1	92	-2.649	44.788	48.100	1.00	0.00
ATOM	837	CD	GLN	1	92	-3.525	44.132	47.065	1.00	0.00
ATOM	838	OE1	GLN	1	92	-3.152	43.262	46.300	1.00	0.00
ATOM	839	NE2	GLN	1	92	-4.730	44.710	46.949	1.00	0.00

Figure 1(con't)

ATOM	840	H	GLN	1	92	-1.391	48.636	47.050	1.00	0.00
ATOM	841	1HE2	GLN	1	92	-5.066	45.404	47.585	1.00	0.00
ATOM	842	2HE2	GLN	1	92	-5.388	44.626	46.200	1.00	0.00
ATOM	843	N	TRP	1	93	0.004	46.795	50.177	1.00	0.00
ATOM	844	CA	TRP	1	93	1.331	46.337	50.664	1.00	0.00
ATOM	845	C	TRP	1	93	1.379	44.847	50.786	1.00	0.00
ATOM	846	O	TRP	1	93	1.413	44.260	51.903	1.00	0.00
ATOM	847	CB	TRP	1	93	1.747	47.092	51.956	1.00	0.00
ATOM	848	CG	TRP	1	93	3.202	46.849	52.298	1.00	0.00
ATOM	849	CD1	TRP	1	93	3.639	46.472	53.600	1.00	0.00
ATOM	850	CD2	TRP	1	93	4.403	46.830	51.462	1.00	0.00
ATOM	851	NE1	TRP	1	93	4.988	46.241	53.629	1.00	0.00
ATOM	852	CE2	TRP	1	93	5.507	46.452	52.349	1.00	0.00
ATOM	853	CE3	TRP	1	93	4.729	47.037	50.081	1.00	0.00
ATOM	854	CZ2	TRP	1	93	6.827	46.319	51.969	1.00	0.00
ATOM	855	CZ3	TRP	1	93	6.089	46.803	49.652	1.00	0.00
ATOM	856	CH2	TRP	1	93	7.087	46.544	50.614	1.00	0.00
ATOM	857	H	TRP	1	93	-0.649	47.178	50.831	1.00	0.00
ATOM	858	1HE	TRP	1	93	5.547	46.033	54.407	1.00	0.00
ATOM	859	N	SER	1	94	1.490	44.234	49.587	1.00	0.00
ATOM	860	CA	SER	1	94	1.669	42.774	49.495	1.00	0.00
ATOM	861	C	SER	1	94	2.312	42.502	48.181	1.00	0.00
ATOM	862	O	SER	1	94	1.754	42.899	47.152	1.00	0.00
ATOM	863	CB	SER	1	94	0.262	42.108	49.593	1.00	0.00
ATOM	864	OG	SER	1	94	-0.412	42.387	48.358	1.00	0.00
ATOM	865	H	SER	1	94	1.514	44.787	48.753	1.00	0.00
ATOM	866	HG	SER	1	94	-0.092	43.219	48.036	1.00	0.00
ATOM	867	N	PRO	1	95	3.435	41.722	48.161	1.00	0.00
ATOM	868	CA	PRO	1	95	3.724	41.167	46.814	1.00	0.00
ATOM	869	C	PRO	1	95	2.942	39.914	46.539	1.00	0.00
ATOM	870	O	PRO	1	95	3.473	38.913	46.075	1.00	0.00
ATOM	871	CB	PRO	1	95	5.243	40.974	46.986	1.00	0.00
ATOM	872	CG	PRO	1	95	5.541	40.527	48.437	1.00	0.00
ATOM	873	CD	PRO	1	95	4.449	41.477	49.162	1.00	0.00
ATOM	874	N	ALA	1	96	1.631	39.963	46.751	1.00	0.00
ATOM	875	CA	ALA	1	96	0.742	38.929	46.296	1.00	0.00
ATOM	876	C	ALA	1	96	0.008	39.214	45.017	1.00	0.00
ATOM	877	O	ALA	1	96	-1.215	39.302	44.930	1.00	0.00
ATOM	878	CB	ALA	1	96	-0.170	38.368	47.410	1.00	0.00
ATOM	879	H	ALA	1	96	1.330	40.893	46.964	1.00	0.00
ATOM	880	N	LEU	1	97	0.914	39.429	44.050	1.00	0.00
ATOM	881	CA	LEU	1	97	0.494	39.917	42.699	1.00	0.00
ATOM	882	C	LEU	1	97	0.773	38.935	41.618	1.00	0.00
ATOM	883	O	LEU	1	97	1.827	38.934	40.926	1.00	0.00
ATOM	884	CB	LEU	1	97	1.151	41.281	42.350	1.00	0.00
ATOM	885	CG	LEU	1	97	1.297	42.490	43.278	1.00	0.00
ATOM	886	CD1	LEU	1	97	1.815	43.697	42.585	1.00	0.00
ATOM	887	CD2	LEU	1	97	-0.071	42.794	44.045	1.00	0.00
ATOM	888	H	LEU	1	97	1.874	39.401	44.330	1.00	0.00
ATOM	889	N	THR	1	98	-0.195	38.052	41.512	1.00	0.00
ATOM	890	CA	THR	1	98	-0.030	37.084	40.473	1.00	0.00
ATOM	891	C	THR	1	98	-0.990	37.340	39.335	1.00	0.00
ATOM	892	O	THR	1	98	-2.041	37.953	39.480	1.00	0.00
ATOM	893	CB	THR	1	98	-0.163	35.572	41.034	1.00	0.00
ATOM	894	OG1	THR	1	98	0.762	34.750	40.274	1.00	0.00
ATOM	895	CG2	THR	1	98	-1.504	35.029	41.173	1.00	0.00

Figure 1(con't)

ATOM	896	H	THR	1	98	-1.027	38.138	42.060	1.00	0.00
ATOM	897	1HG	THR	1	98	0.266	34.090	39.808	1.00	0.00
ATOM	898	N	ILE	1	99	-0.363	37.052	38.234	1.00	0.00
ATOM	899	CA	ILE	1	99	-0.894	37.527	37.020	1.00	0.00
ATOM	900	C	ILE	1	99	-2.380	37.698	36.697	1.00	0.00
ATOM	901	O	ILE	1	99	-2.724	38.764	36.246	1.00	0.00
ATOM	902	CB	ILE	1	99	-0.082	37.024	35.825	1.00	0.00
ATOM	903	CG1	ILE	1	99	-0.308	37.613	34.450	1.00	0.00
ATOM	904	CG2	ILE	1	99	-0.305	35.483	35.600	1.00	0.00
ATOM	905	CD1	ILE	1	99	0.494	38.884	34.205	1.00	0.00
ATOM	906	H	ILE	1	99	0.345	36.354	38.343	1.00	0.00
ATOM	907	N	SER	1	100	-3.270	36.706	36.849	1.00	0.00
ATOM	908	CA	SER	1	100	-4.724	36.906	36.744	1.00	0.00
ATOM	909	C	SER	1	100	-5.204	38.211	37.355	1.00	0.00
ATOM	910	O	SER	1	100	-5.742	39.096	36.685	1.00	0.00
ATOM	911	CB	SER	1	100	-5.415	35.624	37.222	1.00	0.00
ATOM	912	OG	SER	1	100	-4.736	35.233	38.459	1.00	0.00
ATOM	913	H	SER	1	100	-2.868	35.938	37.348	1.00	0.00
ATOM	914	HG	SER	1	100	-5.204	34.561	38.936	1.00	0.00
ATOM	915	N	LYS	1	101	-4.768	38.359	38.639	1.00	0.00
ATOM	916	CA	LYS	1	101	-5.113	39.564	39.413	1.00	0.00
ATOM	917	C	LYS	1	101	-4.402	40.879	39.024	1.00	0.00
ATOM	918	O	LYS	1	101	-4.754	41.953	39.522	1.00	0.00
ATOM	919	CB	LYS	1	101	-4.912	39.238	40.866	1.00	0.00
ATOM	920	CG	LYS	1	101	-5.274	40.259	42.002	1.00	0.00
ATOM	921	CD	LYS	1	101	-3.984	40.688	42.680	1.00	0.00
ATOM	922	CE	LYS	1	101	-4.365	40.819	44.136	1.00	0.00
ATOM	923	NZ	LYS	1	101	-3.203	41.272	44.871	1.00	0.00
ATOM	924	H	LYS	1	101	-4.189	37.616	38.973	1.00	0.00
ATOM	925	1HZ	LYS	1	101	-2.880	42.183	44.487	1.00	0.00
ATOM	926	2HZ	LYS	1	101	-3.296	41.474	45.887	1.00	0.00
ATOM	927	3HZ	LYS	1	101	-2.424	40.594	44.747	1.00	0.00
ATOM	928	N	VAL	1	102	-3.475	40.750	38.077	1.00	0.00
ATOM	929	CA	VAL	1	102	-2.860	41.961	37.557	1.00	0.00
ATOM	930	C	VAL	1	102	-3.510	42.388	36.239	1.00	0.00
ATOM	931	O	VAL	1	102	-3.849	43.567	35.957	1.00	0.00
ATOM	932	CB	VAL	1	102	-1.348	41.798	37.381	1.00	0.00
ATOM	933	CG1	VAL	1	102	-0.665	43.196	37.067	1.00	0.00
ATOM	934	CG2	VAL	1	102	-0.609	41.199	38.633	1.00	0.00
ATOM	935	H	VAL	1	102	-3.259	39.834	37.736	1.00	0.00
ATOM	936	N	LEU	1	103	-3.744	41.406	35.354	1.00	0.00
ATOM	937	CA	LEU	1	103	-4.192	41.772	34.076	1.00	0.00
ATOM	938	C	LEU	1	103	-5.690	42.032	34.111	1.00	0.00
ATOM	939	O	LEU	1	103	-6.211	42.990	33.448	1.00	0.00
ATOM	940	CB	LEU	1	103	-3.726	40.740	32.995	1.00	0.00
ATOM	941	CG	LEU	1	103	-2.507	41.346	32.267	1.00	0.00
ATOM	942	CD1	LEU	1	103	-1.795	40.254	31.459	1.00	0.00
ATOM	943	CD2	LEU	1	103	-2.903	42.587	31.541	1.00	0.00
ATOM	944	H	LEU	1	103	-3.911	40.514	35.773	1.00	0.00
ATOM	945	N	LEU	1	104	-6.424	41.145	34.856	1.00	0.00
ATOM	946	CA	LEU	1	104	-7.810	41.575	35.127	1.00	0.00
ATOM	947	C	LEU	1	104	-7.855	42.961	35.724	1.00	0.00
ATOM	948	O	LEU	1	104	-8.500	43.819	35.130	1.00	0.00
ATOM	949	CB	LEU	1	104	-8.506	40.520	35.983	1.00	0.00
ATOM	950	CG	LEU	1	104	-9.953	40.895	36.094	1.00	0.00
ATOM	951	CD1	LEU	1	104	-10.722	40.812	34.846	1.00	0.00

Figure 1(con't)

ATOM	952	CD2	LEU	1	104	-10.702	40.028	37.125	1.00	0.00
ATOM	953	H	LEU	1	104	-6.131	40.287	35.278	1.00	0.00
ATOM	954	N	SER	1	105	-7.118	43.132	36.833	1.00	0.00
ATOM	955	CA	SER	1	105	-7.386	44.418	37.550	1.00	0.00
ATOM	956	C	SER	1	105	-6.973	45.720	36.778	1.00	0.00
ATOM	957	O	SER	1	105	-7.602	46.737	36.986	1.00	0.00
ATOM	958	CB	SER	1	105	-6.761	44.419	38.909	1.00	0.00
ATOM	959	OG	SER	1	105	-7.437	43.369	39.676	1.00	0.00
ATOM	960	H	SER	1	105	-6.570	42.378	37.194	1.00	0.00
ATOM	961	HG	SER	1	105	-7.053	42.532	39.449	1.00	0.00
ATOM	962	N	ILE	1	106	-5.953	45.587	35.942	1.00	0.00
ATOM	963	CA	ILE	1	106	-5.565	46.649	34.950	1.00	0.00
ATOM	964	C	ILE	1	106	-6.694	46.937	33.906	1.00	0.00
ATOM	965	O	ILE	1	106	-7.039	48.044	33.459	1.00	0.00
ATOM	966	CB	ILE	1	106	-4.240	46.330	34.320	1.00	0.00
ATOM	967	CG1	ILE	1	106	-3.013	46.371	35.246	1.00	0.00
ATOM	968	CG2	ILE	1	106	-3.926	47.235	33.094	1.00	0.00
ATOM	969	CD1	ILE	1	106	-1.919	45.558	34.629	1.00	0.00
ATOM	970	H	ILE	1	106	-5.752	44.610	35.861	1.00	0.00
ATOM	971	N	CYS	1	107	-7.274	45.781	33.409	1.00	0.00
ATOM	972	CA	CYS	1	107	-8.520	45.970	32.586	1.00	0.00
ATOM	973	C	CYS	1	107	-9.757	46.433	33.338	1.00	0.00
ATOM	974	O	CYS	1	107	-10.600	47.145	32.731	1.00	0.00
ATOM	975	CB	CYS	1	107	-8.856	44.670	31.741	1.00	0.00
ATOM	976	SG	CYS	1	107	-7.429	44.342	30.720	1.00	0.00
ATOM	977	H	CYS	1	107	-7.117	44.941	33.928	1.00	0.00
ATOM	978	N	SER	1	108	-9.830	46.108	34.695	1.00	0.00
ATOM	979	CA	SER	1	108	-11.060	46.479	35.328	1.00	0.00
ATOM	980	C	SER	1	108	-11.219	47.952	35.369	1.00	0.00
ATOM	981	O	SER	1	108	-12.337	48.405	35.150	1.00	0.00
ATOM	982	CB	SER	1	108	-11.152	45.799	36.770	1.00	0.00
ATOM	983	OG	SER	1	108	-11.173	44.322	36.587	1.00	0.00
ATOM	984	H	SER	1	108	-9.241	45.357	34.994	1.00	0.00
ATOM	985	HG	SER	1	108	-11.732	44.168	35.837	1.00	0.00
ATOM	986	N	LEU	1	109	-10.155	48.631	35.780	1.00	0.00
ATOM	987	CA	LEU	1	109	-10.220	50.104	35.653	1.00	0.00
ATOM	988	C	LEU	1	109	-9.817	50.687	34.332	1.00	0.00
ATOM	989	O	LEU	1	109	-9.444	51.821	34.154	1.00	0.00
ATOM	990	CB	LEU	1	109	-9.558	50.849	36.830	1.00	0.00
ATOM	991	CG	LEU	1	109	-10.330	50.611	38.192	1.00	0.00
ATOM	992	CD1	LEU	1	109	-9.530	51.170	39.297	1.00	0.00
ATOM	993	CD2	LEU	1	109	-11.727	51.119	38.162	1.00	0.00
ATOM	994	H	LEU	1	109	-9.232	48.266	35.900	1.00	0.00
ATOM	995	N	LEU	1	110	-9.934	49.766	33.374	1.00	0.00
ATOM	996	CA	LEU	1	110	-10.049	50.216	32.023	1.00	0.00
ATOM	997	C	LEU	1	110	-11.371	49.745	31.298	1.00	0.00
ATOM	998	O	LEU	1	110	-11.455	49.615	30.102	1.00	0.00
ATOM	999	CB	LEU	1	110	-8.751	49.816	31.312	1.00	0.00
ATOM	1000	CG	LEU	1	110	-7.942	50.875	30.483	1.00	0.00
ATOM	1001	CD1	LEU	1	110	-7.368	51.879	31.470	1.00	0.00
ATOM	1002	CD2	LEU	1	110	-6.829	50.314	29.656	1.00	0.00
ATOM	1003	H	LEU	1	110	-10.041	48.784	33.533	1.00	0.00
ATOM	1004	N	CYS	1	111	-12.308	49.338	32.152	1.00	0.00
ATOM	1005	CA	CYS	1	111	-13.548	48.999	31.551	1.00	0.00
ATOM	1006	C	CYS	1	111	-14.398	50.255	31.331	1.00	0.00
ATOM	1007	O	CYS	1	111	-14.130	50.937	30.370	1.00	0.00

Figure 1(con't)

ATOM	1008	CB	CYS	1	111	-14.416	48.026	32.492	1.00	0.00
ATOM	1009	SG	CYS	1	111	-14.116	46.278	32.379	1.00	0.00
ATOM	1010	H	CYS	1	111	-12.026	49.328	33.112	1.00	0.00
ATOM	1011	N	ASP	1	112	-15.364	50.587	32.178	1.00	0.00
ATOM	1012	CA	ASP	1	112	-15.593	51.987	32.403	1.00	0.00
ATOM	1013	C	ASP	1	112	-14.518	52.650	33.331	1.00	0.00
ATOM	1014	O	ASP	1	112	-14.507	52.386	34.545	1.00	0.00
ATOM	1015	CB	ASP	1	112	-17.121	52.182	32.807	1.00	0.00
ATOM	1016	CG	ASP	1	112	-17.888	52.937	31.766	1.00	0.00
ATOM	1017	OD1	ASP	1	112	-19.113	52.989	31.785	1.00	0.00
ATOM	1018	OD2	ASP	1	112	-17.199	53.537	30.912	1.00	0.00
ATOM	1019	H	ASP	1	112	-15.765	49.992	32.874	1.00	0.00
ATOM	1020	N	PRO	1	113	-13.531	53.288	32.615	1.00	0.00
ATOM	1021	CA	PRO	1	113	-12.199	53.281	33.187	1.00	0.00
ATOM	1022	C	PRO	1	113	-12.012	54.384	34.243	1.00	0.00
ATOM	1023	O	PRO	1	113	-12.637	55.445	34.025	1.00	0.00
ATOM	1024	CB	PRO	1	113	-11.398	53.419	31.897	1.00	0.00
ATOM	1025	CG	PRO	1	113	-12.171	54.275	30.881	1.00	0.00
ATOM	1026	CD	PRO	1	113	-13.610	53.875	31.275	1.00	0.00
ATOM	1027	N	ASN	1	114	-11.261	54.180	35.336	1.00	0.00
ATOM	1028	CA	ASN	1	114	-11.182	55.245	36.355	1.00	0.00
ATOM	1029	C	ASN	1	114	-10.597	56.637	35.865	1.00	0.00
ATOM	1030	O	ASN	1	114	-9.378	56.803	35.714	1.00	0.00
ATOM	1031	CB	ASN	1	114	-10.330	54.764	37.541	1.00	0.00
ATOM	1032	CG	ASN	1	114	-10.137	55.772	38.647	1.00	0.00
ATOM	1033	OD1	ASN	1	114	-9.345	56.731	38.656	1.00	0.00
ATOM	1034	ND2	ASN	1	114	-10.980	55.677	39.678	1.00	0.00
ATOM	1035	H	ASN	1	114	-10.615	53.417	35.332	1.00	0.00
ATOM	1036	1HD2	ASN	1	114	-11.523	54.841	39.754	1.00	0.00
ATOM	1037	2HD2	ASN	1	114	-11.318	56.332	40.354	1.00	0.00
ATOM	1038	N	PRO	1	115	-11.568	57.547	35.930	1.00	0.00
ATOM	1039	CA	PRO	1	115	-11.202	58.938	35.634	1.00	0.00
ATOM	1040	C	PRO	1	115	-10.529	59.625	36.725	1.00	0.00
ATOM	1041	O	PRO	1	115	-9.921	60.690	36.497	1.00	0.00
ATOM	1042	CB	PRO	1	115	-12.673	59.470	35.330	1.00	0.00
ATOM	1043	CG	PRO	1	115	-13.720	58.740	36.127	1.00	0.00
ATOM	1044	CD	PRO	1	115	-12.975	57.417	36.159	1.00	0.00
ATOM	1045	N	ASP	1	116	-10.763	59.056	37.948	1.00	0.00
ATOM	1046	CA	ASP	1	116	-10.371	59.852	39.097	1.00	0.00
ATOM	1047	C	ASP	1	116	-8.965	60.130	39.381	1.00	0.00
ATOM	1048	O	ASP	1	116	-8.729	61.091	40.080	1.00	0.00
ATOM	1049	CB	ASP	1	116	-11.112	59.169	40.210	1.00	0.00
ATOM	1050	CG	ASP	1	116	-12.562	59.525	40.004	1.00	0.00
ATOM	1051	OD1	ASP	1	116	-12.897	60.693	40.229	1.00	0.00
ATOM	1052	OD2	ASP	1	116	-13.360	58.645	39.645	1.00	0.00
ATOM	1053	H	ASP	1	116	-11.087	58.122	38.101	1.00	0.00
ATOM	1054	N	ASP	1	117	-8.046	59.379	38.889	1.00	0.00
ATOM	1055	CA	ASP	1	117	-6.667	59.696	39.115	1.00	0.00
ATOM	1056	C	ASP	1	117	-6.000	60.362	37.956	1.00	0.00
ATOM	1057	O	ASP	1	117	-5.912	59.906	36.817	1.00	0.00
ATOM	1058	CB	ASP	1	117	-5.812	58.462	39.672	1.00	0.00
ATOM	1059	CG	ASP	1	117	-5.071	58.862	40.969	1.00	0.00
ATOM	1060	OD1	ASP	1	117	-5.706	59.224	41.919	1.00	0.00
ATOM	1061	OD2	ASP	1	117	-3.839	58.861	40.982	1.00	0.00
ATOM	1062	H	ASP	1	117	-8.297	58.676	38.225	1.00	0.00
ATOM	1063	N	PRO	1	118	-5.510	61.616	38.265	1.00	0.00

Figure 1(con't)

ATOM	1064	CA	PRO	1	118	-4.974	62.450	37.154	1.00	0.00
ATOM	1065	C	PRO	1	118	-3.551	62.218	36.754	1.00	0.00
ATOM	1066	O	PRO	1	118	-2.677	63.093	36.734	1.00	0.00
ATOM	1067	CB	PRO	1	118	-5.149	63.800	37.805	1.00	0.00
ATOM	1068	CG	PRO	1	118	-4.936	63.597	39.311	1.00	0.00
ATOM	1069	CD	PRO	1	118	-5.578	62.267	39.561	1.00	0.00
ATOM	1070	N	LEU	1	119	-3.257	60.906	36.463	1.00	0.00
ATOM	1071	CA	LEU	1	119	-1.905	60.688	35.982	1.00	0.00
ATOM	1072	C	LEU	1	119	-1.307	61.479	34.745	1.00	0.00
ATOM	1073	O	LEU	1	119	-0.441	62.318	34.908	1.00	0.00
ATOM	1074	CB	LEU	1	119	-1.456	59.254	35.930	1.00	0.00
ATOM	1075	CG	LEU	1	119	-1.532	58.349	37.167	1.00	0.00
ATOM	1076	CD1	LEU	1	119	-0.912	56.912	36.972	1.00	0.00
ATOM	1077	CD2	LEU	1	119	-0.790	58.990	38.341	1.00	0.00
ATOM	1078	H	LEU	1	119	-3.921	60.164	36.368	1.00	0.00
ATOM	1079	N	VAL	1	120	-1.971	61.216	33.617	1.00	0.00
ATOM	1080	CA	VAL	1	120	-1.959	62.209	32.538	1.00	0.00
ATOM	1081	C	VAL	1	120	-3.329	62.894	32.518	1.00	0.00
ATOM	1082	O	VAL	1	120	-4.360	62.293	32.613	1.00	0.00
ATOM	1083	CB	VAL	1	120	-1.499	61.604	31.253	1.00	0.00
ATOM	1084	CG1	VAL	1	120	0.035	61.659	31.162	1.00	0.00
ATOM	1085	CG2	VAL	1	120	-2.097	60.128	30.928	1.00	0.00
ATOM	1086	H	VAL	1	120	-2.662	60.500	33.718	1.00	0.00
ATOM	1087	N	PRO	1	121	-3.277	64.280	32.514	1.00	0.00
ATOM	1088	CA	PRO	1	121	-4.501	65.112	32.553	1.00	0.00
ATOM	1089	C	PRO	1	121	-5.183	65.158	31.223	1.00	0.00
ATOM	1090	O	PRO	1	121	-5.005	66.142	30.408	1.00	0.00
ATOM	1091	CB	PRO	1	121	-4.078	66.545	32.890	1.00	0.00
ATOM	1092	CG	PRO	1	121	-2.593	66.574	32.951	1.00	0.00
ATOM	1093	CD	PRO	1	121	-2.099	65.167	32.581	1.00	0.00
ATOM	1094	N	GLU	1	122	-5.946	64.072	30.888	1.00	0.00
ATOM	1095	CA	GLU	1	122	-6.357	64.028	29.506	1.00	0.00
ATOM	1096	C	GLU	1	122	-7.790	64.010	29.329	1.00	0.00
ATOM	1097	O	GLU	1	122	-8.390	64.999	28.991	1.00	0.00
ATOM	1098	CB	GLU	1	122	-5.562	62.967	28.680	1.00	0.00
ATOM	1099	CG	GLU	1	122	-5.508	61.536	29.110	1.00	0.00
ATOM	1100	CD	GLU	1	122	-4.428	60.841	28.287	1.00	0.00
ATOM	1101	OE1	GLU	1	122	-4.533	59.662	28.084	1.00	0.00
ATOM	1102	OE2	GLU	1	122	-3.419	61.458	27.964	1.00	0.00
ATOM	1103	H	GLU	1	122	-5.977	63.325	31.552	1.00	0.00
ATOM	1104	N	ILE	1	123	-8.356	62.858	29.591	1.00	0.00
ATOM	1105	CA	ILE	1	123	-9.817	62.884	29.471	1.00	0.00
ATOM	1106	C	ILE	1	123	-10.637	62.807	30.714	1.00	0.00
ATOM	1107	O	ILE	1	123	-11.593	63.548	30.791	1.00	0.00
ATOM	1108	CB	ILE	1	123	-10.141	61.868	28.403	1.00	0.00
ATOM	1109	CG1	ILE	1	123	-11.547	62.072	27.779	1.00	0.00
ATOM	1110	CG2	ILE	1	123	-10.056	60.403	28.786	1.00	0.00
ATOM	1111	CD1	ILE	1	123	-11.761	63.221	26.711	1.00	0.00
ATOM	1112	H	ILE	1	123	-7.841	62.124	30.034	1.00	0.00
ATOM	1113	N	ALA	1	124	-10.185	61.872	31.630	1.00	0.00
ATOM	1114	CA	ALA	1	124	-10.610	61.878	33.046	1.00	0.00
ATOM	1115	C	ALA	1	124	-12.162	62.048	33.276	1.00	0.00
ATOM	1116	O	ALA	1	124	-13.048	61.516	32.542	1.00	0.00
ATOM	1117	CB	ALA	1	124	-9.795	63.009	33.690	1.00	0.00
ATOM	1118	H	ALA	1	124	-9.351	61.353	31.444	1.00	0.00
ATOM	1119	N	ARG	1	125	-12.434	62.735	34.377	1.00	0.00

Figure 1(con't)

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ATOM   1120  CA  ARG 1  125      -13.795  63.212  34.682  1.00  0.00
ATOM   1121  C   ARG 1  125      -14.747  63.817  33.616  1.00  0.00
ATOM   1122  O   ARG 1  125      -15.960  63.759  33.744  1.00  0.00
ATOM   1123  CB  ARG 1  125      -13.769  64.204  35.773  1.00  0.00
ATOM   1124  CG  ARG 1  125      -13.675  63.377  37.072  1.00  0.00
ATOM   1125  CD  ARG 1  125      -14.972  62.537  37.191  1.00  0.00
ATOM   1126  NE  ARG 1  125      -14.854  61.500  38.232  1.00  0.00
ATOM   1127  CZ  ARG 1  125      -15.861  60.967  38.847  1.00  0.00
ATOM   1128  NH1 ARG 1  125      -15.655  59.990  39.749  1.00  0.00
ATOM   1129  NH2 ARG 1  125      -17.122  61.349  38.534  1.00  0.00
ATOM   1130  H   ARG 1  125      -11.855  63.259  35.001  1.00  0.00
ATOM   1131  HE  ARG 1  125      -13.919  61.221  38.454  1.00  0.00
ATOM   1132 1HH1 ARG 1  125      -16.416  59.493  40.167  1.00  0.00
ATOM   1133 2HH1 ARG 1  125      -14.748  59.735  40.086  1.00  0.00
ATOM   1134 1HH2 ARG 1  125      -17.856  61.089  39.162  1.00  0.00
ATOM   1135 2HH2 ARG 1  125      -17.314  61.932  37.745  1.00  0.00
ATOM   1136  N   ILE 1  126      -14.127  64.432  32.608  1.00  0.00
ATOM   1137  CA  ILE 1  126      -14.788  64.980  31.466  1.00  0.00
ATOM   1138  C   ILE 1  126      -15.410  63.856  30.692  1.00  0.00
ATOM   1139  O   ILE 1  126      -16.523  63.970  30.167  1.00  0.00
ATOM   1140  CB  ILE 1  126      -13.766  65.724  30.522  1.00  0.00
ATOM   1141  CG1 ILE 1  126      -13.082  66.752  31.461  1.00  0.00
ATOM   1142  CG2 ILE 1  126      -14.467  66.385  29.299  1.00  0.00
ATOM   1143  CD1 ILE 1  126      -11.753  67.296  30.873  1.00  0.00
ATOM   1144  H   ILE 1  126      -13.135  64.303  32.601  1.00  0.00
ATOM   1145  N   TYR 1  127      -14.624  62.715  30.636  1.00  0.00
ATOM   1146  CA  TYR 1  127      -15.167  61.452  30.126  1.00  0.00
ATOM   1147  C   TYR 1  127      -16.529  61.083  30.734  1.00  0.00
ATOM   1148  O   TYR 1  127      -17.440  60.554  30.100  1.00  0.00
ATOM   1149  CB  TYR 1  127      -14.051  60.272  30.134  1.00  0.00
ATOM   1150  CG  TYR 1  127      -14.489  59.022  30.878  1.00  0.00
ATOM   1151  CD1 TYR 1  127      -15.254  58.078  30.129  1.00  0.00
ATOM   1152  CD2 TYR 1  127      -14.209  58.796  32.260  1.00  0.00
ATOM   1153  CE1 TYR 1  127      -15.911  56.995  30.838  1.00  0.00
ATOM   1154  CE2 TYR 1  127      -14.809  57.674  32.912  1.00  0.00
ATOM   1155  CZ  TYR 1  127      -15.750  56.817  32.219  1.00  0.00
ATOM   1156  OH  TYR 1  127      -16.381  55.818  32.877  1.00  0.00
ATOM   1157  H   TYR 1  127      -13.751  62.624  31.115  1.00  0.00
ATOM   1158  HH  TYR 1  127      -16.924  55.379  32.236  1.00  0.00
ATOM   1159  N   GLN 1  128      -16.689  61.447  32.006  1.00  0.00
ATOM   1160  CA  GLN 1  128      -17.972  61.076  32.613  1.00  0.00
ATOM   1161  C   GLN 1  128      -18.820  62.307  32.767  1.00  0.00
ATOM   1162  O   GLN 1  128      -19.700  62.437  33.627  1.00  0.00
ATOM   1163  CB  GLN 1  128      -17.573  60.544  33.940  1.00  0.00
ATOM   1164  CG  GLN 1  128      -18.401  59.339  34.361  1.00  0.00
ATOM   1165  CD  GLN 1  128      -17.669  58.576  35.474  1.00  0.00
ATOM   1166  OE1 GLN 1  128      -17.437  59.077  36.587  1.00  0.00
ATOM   1167  NE2 GLN 1  128      -17.060  57.418  35.047  1.00  0.00
ATOM   1168  H   GLN 1  128      -15.933  61.976  32.392  1.00  0.00
ATOM   1169 1HE2 GLN 1  128      -17.400  56.974  34.218  1.00  0.00
ATOM   1170 2HE2 GLN 1  128      -16.287  57.080  35.584  1.00  0.00
ATOM   1171  N   THR 1  129      -18.610  63.261  31.790  1.00  0.00
ATOM   1172  CA  THR 1  129      -19.554  64.402  31.531  1.00  0.00
ATOM   1173  C   THR 1  129      -20.034  64.338  30.090  1.00  0.00
ATOM   1174  O   THR 1  129      -21.188  64.645  29.868  1.00  0.00
ATOM   1175  CB  THR 1  129      -18.694  65.689  31.759  1.00  0.00
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Figure 1(con't)

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ATOM   1176  OG1 THR 1  129      -17.843  65.533  32.883  1.00  0.00
ATOM   1177  CG2 THR 1  129      -19.575  66.877  31.994  1.00  0.00
ATOM   1178  H   THR 1  129      -17.822  63.069  31.205  1.00  0.00
ATOM   1179 1HG  THR 1  129      -17.276  64.776  32.808  1.00  0.00
ATOM   1180  N   ASP 1  130      -19.100  63.839  29.242  1.00  0.00
ATOM   1181  CA  ASP 1  130      -19.272  63.530  27.815  1.00  0.00
ATOM   1182  C   ASP 1  130      -18.547  62.268  27.468  1.00  0.00
ATOM   1183  O   ASP 1  130      -17.360  62.026  27.412  1.00  0.00
ATOM   1184  CB  ASP 1  130      -18.822  64.757  26.978  1.00  0.00
ATOM   1185  CG  ASP 1  130      -18.897  64.631  25.454  1.00  0.00
ATOM   1186  OD1 ASP 1  130      -19.920  64.947  24.888  1.00  0.00
ATOM   1187  OD2 ASP 1  130      -17.905  64.242  24.882  1.00  0.00
ATOM   1188  H   ASP 1  130      -18.255  63.427  29.582  1.00  0.00
ATOM   1189  N   ARG 1  131      -19.410  61.274  27.309  1.00  0.00
ATOM   1190  CA  ARG 1  131      -18.935  59.959  26.768  1.00  0.00
ATOM   1191  C   ARG 1  131      -18.469  60.154  25.366  1.00  0.00
ATOM   1192  O   ARG 1  131      -17.594  59.446  24.815  1.00  0.00
ATOM   1193  CB  ARG 1  131      -20.032  58.855  26.756  1.00  0.00
ATOM   1194  CG  ARG 1  131      -20.416  58.478  28.193  1.00  0.00
ATOM   1195  CD  ARG 1  131      -19.194  57.782  28.955  1.00  0.00
ATOM   1196  NE  ARG 1  131      -18.986  56.441  28.423  1.00  0.00
ATOM   1197  CZ  ARG 1  131      -19.071  55.351  29.184  1.00  0.00
ATOM   1198  NH1 ARG 1  131      -18.900  54.185  28.671  1.00  0.00
ATOM   1199  NH2 ARG 1  131      -19.376  55.517  30.503  1.00  0.00
ATOM   1200  H   ARG 1  131      -20.369  61.548  27.370  1.00  0.00
ATOM   1201  HE  ARG 1  131      -18.632  56.469  27.488  1.00  0.00
ATOM   1202 1HH1 ARG 1  131      -18.956  53.332  29.191  1.00  0.00
ATOM   1203 2HH1 ARG 1  131      -18.792  54.024  27.690  1.00  0.00
ATOM   1204 1HH2 ARG 1  131      -19.481  54.718  31.095  1.00  0.00
ATOM   1205 2HH2 ARG 1  131      -19.542  56.412  30.918  1.00  0.00
ATOM   1206  N   GLU 1  132      -19.073  61.146  24.679  1.00  0.00
ATOM   1207  CA  GLU 1  132      -19.097  61.123  23.223  1.00  0.00
ATOM   1208  C   GLU 1  132      -17.704  61.256  22.550  1.00  0.00
ATOM   1209  O   GLU 1  132      -17.303  60.476  21.676  1.00  0.00
ATOM   1210  CB  GLU 1  132      -20.158  62.165  22.829  1.00  0.00
ATOM   1211  CG  GLU 1  132      -20.663  62.490  21.437  1.00  0.00
ATOM   1212  CD  GLU 1  132      -19.538  62.468  20.507  1.00  0.00
ATOM   1213  OE1 GLU 1  132      -18.751  63.417  20.464  1.00  0.00
ATOM   1214  OE2 GLU 1  132      -19.328  61.449  19.842  1.00  0.00
ATOM   1215  H   GLU 1  132      -19.447  61.944  25.151  1.00  0.00
ATOM   1216  N   LYS 1  133      -16.973  62.276  23.084  1.00  0.00
ATOM   1217  CA  LYS 1  133      -15.616  62.452  22.586  1.00  0.00
ATOM   1218  C   LYS 1  133      -14.629  61.391  22.856  1.00  0.00
ATOM   1219  O   LYS 1  133      -13.837  60.980  22.044  1.00  0.00
ATOM   1220  CB  LYS 1  133      -15.115  63.846  22.950  1.00  0.00
ATOM   1221  CG  LYS 1  133      -15.678  64.917  22.035  1.00  0.00
ATOM   1222  CD  LYS 1  133      -16.243  66.106  22.825  1.00  0.00
ATOM   1223  CE  LYS 1  133      -17.623  66.499  22.255  1.00  0.00
ATOM   1224  NZ  LYS 1  133      -18.680  65.449  22.455  1.00  0.00
ATOM   1225  H   LYS 1  133      -17.198  62.759  23.930  1.00  0.00
ATOM   1226 1HZ  LYS 1  133      -18.725  64.799  21.645  1.00  0.00
ATOM   1227 2HZ  LYS 1  133      -18.439  64.912  23.313  1.00  0.00
ATOM   1228 3HZ  LYS 1  133      -19.642  65.786  22.663  1.00  0.00
ATOM   1229  N   TYR 1  134      -14.790  60.794  24.068  1.00  0.00
ATOM   1230  CA  TYR 1  134      -14.077  59.548  24.365  1.00  0.00
ATOM   1231  C   TYR 1  134      -14.477  58.281  23.495  1.00  0.00
```

Figure 1(con't)

```
ATOM   1232  O   TYR 1  134      -13.564  57.463  23.191  1.00  0.00
ATOM   1233  CB  TYR 1  134      -14.163  59.285  25.901  1.00  0.00
ATOM   1234  CG  TYR 1  134      -13.902  57.807  26.279  1.00  0.00
ATOM   1235  CD1 TYR 1  134      -12.616  57.238  26.234  1.00  0.00
ATOM   1236  CD2 TYR 1  134      -14.952  56.954  26.703  1.00  0.00
ATOM   1237  CE1 TYR 1  134      -12.308  55.950  26.691  1.00  0.00
ATOM   1238  CE2 TYR 1  134      -14.739  55.641  27.144  1.00  0.00
ATOM   1239  CZ  TYR 1  134      -13.388  55.147  27.137  1.00  0.00
ATOM   1240  OH  TYR 1  134      -13.089  53.833  27.509  1.00  0.00
ATOM   1241  H   TYR 1  134      -15.605  61.016  24.604  1.00  0.00
ATOM   1242  HH  TYR 1  134      -12.629  53.955  28.329  1.00  0.00
ATOM   1243  N   ASN 1  135      -15.732  58.290  23.026  1.00  0.00
ATOM   1244  CA  ASN 1  135      -16.023  57.578  21.793  1.00  0.00
ATOM   1245  C   ASN 1  135      -15.345  58.003  20.446  1.00  0.00
ATOM   1246  O   ASN 1  135      -16.007  57.968  19.385  1.00  0.00
ATOM   1247  CB  ASN 1  135      -17.458  57.139  21.710  1.00  0.00
ATOM   1248  CG  ASN 1  135      -17.585  55.762  22.262  1.00  0.00
ATOM   1249  OD1 ASN 1  135      -17.810  55.462  23.457  1.00  0.00
ATOM   1250  ND2 ASN 1  135      -17.359  54.819  21.344  1.00  0.00
ATOM   1251  H   ASN 1  135      -16.422  58.886  23.436  1.00  0.00
ATOM   1252 1HD2 ASN 1  135      -17.077  54.977  20.398  1.00  0.00
ATOM   1253 2HD2 ASN 1  135      -17.430  53.873  21.660  1.00  0.00
ATOM   1254  N   ARG 1  136      -14.053  58.370  20.478  1.00  0.00
ATOM   1255  CA  ARG 1  136      -13.385  58.938  19.318  1.00  0.00
ATOM   1256  C   ARG 1  136      -11.907  59.136  19.706  1.00  0.00
ATOM   1257  O   ARG 1  136      -11.120  58.192  19.624  1.00  0.00
ATOM   1258  CB  ARG 1  136      -13.963  60.323  18.860  1.00  0.00
ATOM   1259  CG  ARG 1  136      -13.759  60.585  17.391  1.00  0.00
ATOM   1260  CD  ARG 1  136      -15.027  60.276  16.539  1.00  0.00
ATOM   1261  NE  ARG 1  136      -16.001  61.343  16.710  1.00  0.00
ATOM   1262  CZ  ARG 1  136      -16.953  61.385  17.722  1.00  0.00
ATOM   1263  NH1 ARG 1  136      -17.634  62.501  17.758  1.00  0.00
ATOM   1264  NH2 ARG 1  136      -17.160  60.427  18.572  1.00  0.00
ATOM   1265  H   ARG 1  136      -13.577  58.270  21.352  1.00  0.00
ATOM   1266  HE  ARG 1  136      -15.978  62.141  16.108  1.00  0.00
ATOM   1267 1HH1 ARG 1  136      -18.194  62.691  18.565  1.00  0.00
ATOM   1268 2HH1 ARG 1  136      -17.585  63.094  16.955  1.00  0.00
ATOM   1269 1HH2 ARG 1  136      -17.955  60.445  19.178  1.00  0.00
ATOM   1270 2HH2 ARG 1  136      -16.527  59.655  18.631  1.00  0.00
ATOM   1271  N   ILE 1  137      -11.553  60.299  20.250  1.00  0.00
ATOM   1272  CA  ILE 1  137      -10.216  60.181  20.894  1.00  0.00
ATOM   1273  C   ILE 1  137      -10.249  59.245  22.086  1.00  0.00
ATOM   1274  O   ILE 1  137      -10.876  59.502  23.085  1.00  0.00
ATOM   1275  CB  ILE 1  137       -9.737  61.669  21.177  1.00  0.00
ATOM   1276  CG1 ILE 1  137      -10.160  62.400  22.437  1.00  0.00
ATOM   1277  CG2 ILE 1  137      -10.058  62.553  19.908  1.00  0.00
ATOM   1278  CD1 ILE 1  137       -9.379  63.684  22.863  1.00  0.00
ATOM   1279  H   ILE 1  137      -12.189  61.029  20.500  1.00  0.00
ATOM   1280  N   ALA 1  138       -9.665  58.091  21.783  1.00  0.00
ATOM   1281  CA  ALA 1  138       -9.599  56.705  22.426  1.00  0.00
ATOM   1282  C   ALA 1  138      -10.195  55.649  21.536  1.00  0.00
ATOM   1283  O   ALA 1  138       -9.601  54.689  21.054  1.00  0.00
ATOM   1284  CB  ALA 1  138      -10.297  56.767  23.804  1.00  0.00
ATOM   1285  H   ALA 1  138       -9.100  58.150  20.960  1.00  0.00
ATOM   1286  N   ARG 1  139      -11.487  55.821  21.280  1.00  0.00
ATOM   1287  CA  ARG 1  139      -11.974  55.035  20.159  1.00  0.00
```

Figure 1(con't)

ATOM	1288	C	ARG	1	139	-11.531	55.522	18.757	1.00	0.00
ATOM	1289	O	ARG	1	139	-12.365	55.995	17.960	1.00	0.00
ATOM	1290	CB	ARG	1	139	-13.446	54.877	20.345	1.00	0.00
ATOM	1291	CG	ARG	1	139	-14.037	53.544	20.350	1.00	0.00
ATOM	1292	CD	ARG	1	139	-13.777	52.739	19.109	1.00	0.00
ATOM	1293	NE	ARG	1	139	-13.294	51.422	19.446	1.00	0.00
ATOM	1294	CZ	ARG	1	139	-14.070	50.451	19.933	1.00	0.00
ATOM	1295	NH1	ARG	1	139	-15.376	50.557	20.176	1.00	0.00
ATOM	1296	NH2	ARG	1	139	-13.546	49.286	20.238	1.00	0.00
ATOM	1297	H	ARG	1	139	-11.953	56.599	21.701	1.00	0.00
ATOM	1298	HE	ARG	1	139	-12.325	51.217	19.312	1.00	0.00
ATOM	1299	1HH1	ARG	1	139	-15.852	49.744	20.511	1.00	0.00
ATOM	1300	2HH1	ARG	1	139	-15.778	51.473	20.172	1.00	0.00
ATOM	1301	1HH2	ARG	1	139	-14.068	48.524	20.623	1.00	0.00
ATOM	1302	2HH2	ARG	1	139	-12.550	49.203	20.209	1.00	0.00
ATOM	1303	N	GLU	1	140	-10.248	55.319	18.431	1.00	0.00
ATOM	1304	CA	GLU	1	140	-9.561	55.842	17.254	1.00	0.00
ATOM	1305	C	GLU	1	140	-8.281	54.950	17.238	1.00	0.00
ATOM	1306	O	GLU	1	140	-8.151	54.134	16.315	1.00	0.00
ATOM	1307	CB	GLU	1	140	-9.381	57.331	17.443	1.00	0.00
ATOM	1308	CG	GLU	1	140	-9.055	58.269	16.321	1.00	0.00
ATOM	1309	CD	GLU	1	140	-7.581	57.782	15.971	1.00	0.00
ATOM	1310	OE1	GLU	1	140	-6.649	57.991	16.665	1.00	0.00
ATOM	1311	OE2	GLU	1	140	-7.440	57.213	14.940	1.00	0.00
ATOM	1312	H	GLU	1	140	-9.824	54.778	19.157	1.00	0.00
ATOM	1313	N	TRP	1	141	-7.528	55.060	18.298	1.00	0.00
ATOM	1314	CA	TRP	1	141	-6.370	54.173	18.571	1.00	0.00
ATOM	1315	C	TRP	1	141	-6.737	52.782	18.944	1.00	0.00
ATOM	1316	O	TRP	1	141	-5.982	51.968	19.452	1.00	0.00
ATOM	1317	CB	TRP	1	141	-5.483	54.663	19.722	1.00	0.00
ATOM	1318	CG	TRP	1	141	-4.774	55.962	19.326	1.00	0.00
ATOM	1319	CD1	TRP	1	141	-3.685	56.131	18.409	1.00	0.00
ATOM	1320	CD2	TRP	1	141	-5.095	57.289	19.700	1.00	0.00
ATOM	1321	NE1	TRP	1	141	-3.327	57.468	18.247	1.00	0.00
ATOM	1322	CE2	TRP	1	141	-4.213	58.240	19.050	1.00	0.00
ATOM	1323	CE3	TRP	1	141	-6.038	57.792	20.591	1.00	0.00
ATOM	1324	CZ2	TRP	1	141	-4.413	59.642	19.300	1.00	0.00
ATOM	1325	CZ3	TRP	1	141	-6.247	59.169	20.883	1.00	0.00
ATOM	1326	CH2	TRP	1	141	-5.415	60.068	20.154	1.00	0.00
ATOM	1327	H	TRP	1	141	-7.623	55.892	18.845	1.00	0.00
ATOM	1328	1HE	TRP	1	141	-2.570	57.837	17.746	1.00	0.00
ATOM	1329	N	THR	1	142	-7.945	52.388	18.669	1.00	0.00
ATOM	1330	CA	THR	1	142	-8.470	51.003	18.796	1.00	0.00
ATOM	1331	C	THR	1	142	-8.785	50.384	17.443	1.00	0.00
ATOM	1332	O	THR	1	142	-8.951	49.195	17.303	1.00	0.00
ATOM	1333	CB	THR	1	142	-9.836	51.112	19.635	1.00	0.00
ATOM	1334	OG1	THR	1	142	-10.085	52.512	20.129	1.00	0.00
ATOM	1335	CG2	THR	1	142	-9.646	50.189	20.902	1.00	0.00
ATOM	1336	H	THR	1	142	-8.557	53.070	18.268	1.00	0.00
ATOM	1337	1HG	THR	1	142	-9.297	52.761	20.593	1.00	0.00
ATOM	1338	N	GLN	1	143	-8.798	51.237	16.420	1.00	0.00
ATOM	1339	CA	GLN	1	143	-8.800	50.759	15.056	1.00	0.00
ATOM	1340	C	GLN	1	143	-7.468	50.990	14.393	1.00	0.00
ATOM	1341	O	GLN	1	143	-6.836	49.990	14.069	1.00	0.00
ATOM	1342	CB	GLN	1	143	-9.874	51.493	14.234	1.00	0.00
ATOM	1343	CG	GLN	1	143	-10.095	50.582	13.074	1.00	0.00

Figure 1(con't)

```
ATOM   1344  CD  GLN 1  143     -10.628  51.426  11.972  1.00  0.00
ATOM   1345  OE1 GLN 1  143     -11.716  51.960  12.091  1.00  0.00
ATOM   1346  NE2 GLN 1  143      -9.832  51.593  10.953  1.00  0.00
ATOM   1347  H   GLN 1  143      -8.441  52.158  16.577  1.00  0.00
ATOM   1348 1HE2 GLN 1  143      -8.858  51.392  10.856  1.00  0.00
ATOM   1349 2HE2 GLN 1  143     -10.262  52.137  10.232  1.00  0.00
ATOM   1350  N   LYS 1  144      -7.185  52.353  14.272  1.00  0.00
ATOM   1351  CA  LYS 1  144      -5.872  52.774  13.923  1.00  0.00
ATOM   1352  C   LYS 1  144      -4.944  52.505  15.064  1.00  0.00
ATOM   1353  O   LYS 1  144      -4.948  53.182  16.090  1.00  0.00
ATOM   1354  CB  LYS 1  144      -6.052  54.219  13.415  1.00  0.00
ATOM   1355  CG  LYS 1  144      -4.756  54.831  12.839  1.00  0.00
ATOM   1356  CD  LYS 1  144      -4.529  56.258  13.351  1.00  0.00
ATOM   1357  CE  LYS 1  144      -4.289  56.135  14.821  1.00  0.00
ATOM   1358  NZ  LYS 1  144      -4.298  57.465  15.486  1.00  0.00
ATOM   1359  H   LYS 1  144      -7.735  53.032  14.760  1.00  0.00
ATOM   1360 1HZ  LYS 1  144      -5.272  57.787  15.657  1.00  0.00
ATOM   1361 2HZ  LYS 1  144      -3.709  57.497  16.342  1.00  0.00
ATOM   1362 3HZ  LYS 1  144      -3.674  58.052  14.895  1.00  0.00
ATOM   1363  N   TYR 1  145      -4.035  51.523  14.725  1.00  0.00
ATOM   1364  CA  TYR 1  145      -2.783  51.563  15.405  1.00  0.00
ATOM   1365  C   TYR 1  145      -1.705  51.911  14.373  1.00  0.00
ATOM   1366  O   TYR 1  145      -1.262  51.077  13.622  1.00  0.00
ATOM   1367  CB  TYR 1  145      -2.651  50.166  16.073  1.00  0.00
ATOM   1368  CG  TYR 1  145      -1.338  50.008  16.760  1.00  0.00
ATOM   1369  CD1 TYR 1  145      -1.119  50.509  18.043  1.00  0.00
ATOM   1370  CD2 TYR 1  145      -0.302  49.394  16.035  1.00  0.00
ATOM   1371  CE1 TYR 1  145       0.150  50.465  18.579  1.00  0.00
ATOM   1372  CE2 TYR 1  145       0.972  49.409  16.589  1.00  0.00
ATOM   1373  CZ  TYR 1  145       1.210  49.922  17.847  1.00  0.00
ATOM   1374  OH  TYR 1  145       2.486  49.934  18.410  1.00  0.00
ATOM   1375  H   TYR 1  145      -4.122  50.802  14.038  1.00  0.00
ATOM   1376  HH  TYR 1  145       2.907  50.776  18.294  1.00  0.00
ATOM   1377  N   ALA 1  146      -1.219  53.200  14.453  1.00  0.00
ATOM   1378  CA  ALA 1  146      -0.018  53.540  13.627  1.00  0.00
ATOM   1379  C   ALA 1  146       0.585  54.832  14.174  1.00  0.00
ATOM   1380  O   ALA 1  146       1.508  54.792  14.958  1.00  0.00
ATOM   1381  CB  ALA 1  146      -0.347  53.708  12.163  1.00  0.00
ATOM   1382  H   ALA 1  146      -1.694  53.960  14.896  1.00  0.00
ATOM   1383  N   MET 1  147       0.146  55.965  13.712  1.00  0.00
ATOM   1384  CA  MET 1  147       0.072  57.199  14.504  1.00  0.00
ATOM   1385  C   MET 1  147      -1.165  57.157  15.439  1.00  0.00
ATOM   1386  O   MET 1  147      -1.746  58.134  15.774  1.00  0.00
ATOM   1387  CB  MET 1  147       0.219  58.444  13.697  1.00  0.00
ATOM   1388  CG  MET 1  147      -0.769  58.439  12.499  1.00  0.00
ATOM   1389  SD  MET 1  147      -0.431  59.820  11.346  1.00  0.00
ATOM   1390  CE  MET 1  147      -2.099  59.928  10.616  1.00  0.00
ATOM   1391  OXT MET 1  147      -1.521  56.064  15.926  1.00  0.00
ATOM   1392  H   MET 1  147      -0.461  55.994  12.919  1.00  0.00
END
```

Figure 2

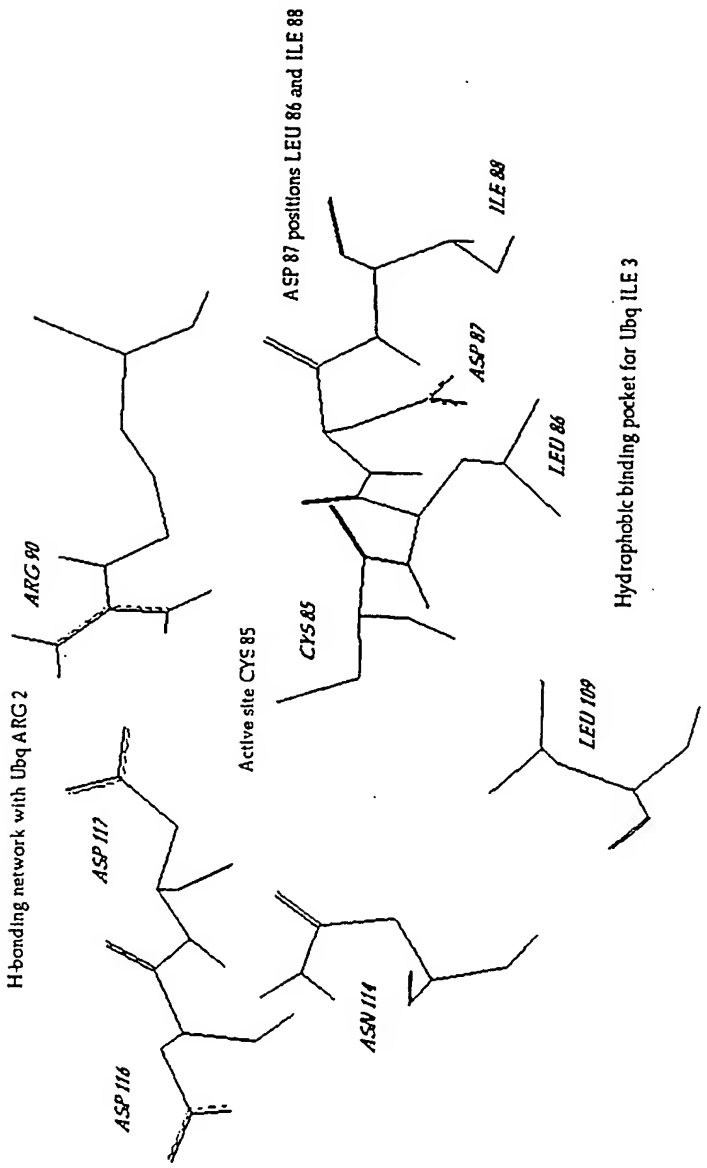

Important residues in ubiquitin binding site in hUCE model
H-bonding network with Ubq ARG 2
ARG 90
ASP 117
ASP 116
Active site CYS 85
CYS 85
ASN 114
ASP 87 positions LEU 86 and ILE 88
ILE 88
ASP 87
LEU 86
LEU 109
Hydrophobic binding pocket for Ubq ILE 3

Figure 3

ATOM	1	N	CYS*1	85	12.813	-15.194	42.441	1.00	0.00
ATOM	2	H	CYS*1	85	13.027	-15.873	41.738	1.00	0.00
ATOM	3	CA	CYS*1	85	13.822	-14.593	43.296	1.00	0.00
ATOM	4	CB	CYS*1	85	14.815	-15.616	43.734	1.00	0.00
ATOM	5	SG	CYS*1	85	15.117	-15.447	45.437	1.00	0.00
ATOM	6	C	CYS*1	85	14.478	-13.341	42.778	1.00	0.00
ATOM	7	O	CYS*1	85	13.994	-12.195	43.023	1.00	0.00
ATOM	8	N	LEU 1	86	15.596	-13.553	42.021	1.00	0.00
ATOM	9	CA	LEU 1	86	16.482	-12.490	41.469	1.00	0.00
ATOM	10	C	LEU 1	86	17.155	-11.557	42.453	1.00	0.00
ATOM	11	O	LEU 1	86	16.664	-11.390	43.514	1.00	0.00
ATOM	12	CB	LEU 1	86	15.850	-11.805	40.281	1.00	0.00
ATOM	13	CG	LEU 1	86	14.624	-12.437	39.580	1.00	0.00
ATOM	14	CD1	LEU 1	86	14.040	-11.515	38.482	1.00	0.00
ATOM	15	CD2	LEU 1	86	14.916	-13.795	38.925	1.00	0.00
ATOM	16	H	LEU 1	86	15.932	-14.493	41.961	1.00	0.00
ATOM	17	N	ASP 1	87	18.301	-10.942	42.020	1.00	0.00
ATOM	18	CA	ASP 1	87	18.887	-9.697	42.577	1.00	0.00
ATOM	19	C	ASP 1	87	17.933	-8.538	42.215	1.00	0.00
ATOM	20	O	ASP 1	87	17.603	-7.688	42.977	1.00	0.00
ATOM	21	CB	ASP 1	87	20.280	-9.473	41.980	1.00	0.00
ATOM	22	CG	ASP 1	87	20.280	-9.437	40.434	1.00	0.00
ATOM	23	OD1	ASP 1	87	21.191	-8.936	39.856	1.00	0.00
ATOM	24	OD2	ASP 1	87	19.409	-9.977	39.792	1.00	0.00
ATOM	25	H	ASP 1	87	18.468	-11.284	41.095	1.00	0.00
ATOM	26	N	ILE 1	88	17.532	-8.458	40.922	1.00	0.00
ATOM	27	CA	ILE 1	88	16.874	-7.254	40.484	1.00	0.00
ATOM	28	C	ILE 1	88	15.486	-7.061	40.987	1.00	0.00
ATOM	29	O	ILE 1	88	14.834	-5.995	40.819	1.00	0.00
ATOM	30	CB	ILE 1	88	16.911	-7.193	38.904	1.00	0.00
ATOM	31	CG1	ILE 1	88	16.078	-8.320	38.291	1.00	0.00
ATOM	32	CG2	ILE 1	88	18.322	-7.055	38.472	1.00	0.00
ATOM	33	CD	ILE 1	88	14.676	-8.014	37.765	1.00	0.00
ATOM	34	H	ILE 1	88	17.739	-9.251	40.349	1.00	0.00
ATOM	35	N	ARG 1	90	14.426	-7.619	44.251	1.00	0.00
ATOM	36	CA	ARG 1	90	14.634	-7.627	45.688	1.00	0.00
ATOM	37	C	ARG 1	90	15.897	-6.845	46.216	1.00	0.00
ATOM	38	O	ARG 1	90	15.818	-5.995	47.079	1.00	0.00
ATOM	39	CB	ARG 1	90	14.624	-9.055	46.305	1.00	0.00
ATOM	40	CG	ARG 1	90	15.765	-10.003	46.039	1.00	0.00
ATOM	41	CD	ARG 1	90	15.221	-11.397	46.218	1.00	0.00
ATOM	42	NE	ARG 1	90	14.864	-11.584	47.622	1.00	0.00
ATOM	43	CZ	ARG 1	90	13.976	-12.617	47.838	1.00	0.00
ATOM	44	NH1	ARG 1	90	13.824	-13.004	49.063	1.00	0.00
ATOM	45	NH2	ARG 1	90	13.426	-13.227	46.779	1.00	0.00
ATOM	46	H	ARG 1	90	14.907	-6.934	43.703	1.00	0.00
ATOM	47	HE	ARG 1	90	15.187	-11.015	48.378	1.00	0.00
ATOM	48	1HH1	ARG 1	90	13.264	-13.807	49.262	1.00	0.00
ATOM	49	2HH1	ARG 1	90	14.153	-12.435	49.817	1.00	0.00
ATOM	50	1HH2	ARG 1	90	12.658	-13.824	47.013	1.00	0.00
ATOM	51	2HH2	ARG 1	90	13.676	-13.086	45.821	1.00	0.00
ATOM	52	N	SER 1	91	17.097	-7.261	45.695	1.00	0.00
ATOM	53	CA	SER 1	91	18.257	-6.643	46.299	1.00	0.00
ATOM	54	C	SER 1	91	19.180	-5.852	45.357	1.00	0.00
ATOM	55	O	SER 1	91	20.364	-5.736	45.486	1.00	0.00
ATOM	56	CB	SER 1	91	19.094	-7.651	47.083	1.00	0.00

Figure 3 (con't)

```
ATOM     57  OG  SER 1  91      18.260  -8.522  47.886  1.00  0.00
ATOM     58  H   SER 1  91      17.222  -7.822  44.876  1.00  0.00
ATOM     59  HG  SER 1  91      17.859  -7.970  48.544  1.00  0.00
ATOM     60  N   LEU 1 109      18.852 -18.359  38.255  1.00  0.00
ATOM     61  CA  LEU 1 109      18.365 -18.942  39.568  1.00  0.00
ATOM     62  C   LEU 1 109      17.179 -19.841  39.495  1.00  0.00
ATOM     63  O   LEU 1 109      16.540 -20.333  40.413  1.00  0.00
ATOM     64  CB  LEU 1 109      18.387 -17.901  40.725  1.00  0.00
ATOM     65  CG  LEU 1 109      19.746 -17.216  40.897  1.00  0.00
ATOM     66  CD1 LEU 1 109      19.834 -15.819  40.391  1.00  0.00
ATOM     67  CD2 LEU 1 109      20.454 -17.598  42.195  1.00  0.00
ATOM     68  H   LEU 1 109      18.274 -17.735  37.728  1.00  0.00
ATOM     69  N   ASN 1 114      17.767 -21.723  43.157  1.00  0.00
ATOM     70  CA  ASN 1 114      17.585 -21.498  44.611  1.00  0.00
ATOM     71  C   ASN 1 114      16.288 -22.097  45.204  1.00  0.00
ATOM     72  O   ASN 1 114      15.110 -21.738  44.968  1.00  0.00
ATOM     73  CB  ASN 1 114      17.738 -20.004  44.811  1.00  0.00
ATOM     74  CG  ASN 1 114      17.761 -19.604  46.263  1.00  0.00
ATOM     75  OD1 ASN 1 114      17.013 -18.825  46.820  1.00  0.00
ATOM     76  ND2 ASN 1 114      18.754 -20.204  46.933  1.00  0.00
ATOM     77  H   ASN 1 114      17.244 -21.387  42.373  1.00  0.00
ATOM     78 1HD2 ASN 1 114      19.381 -20.849  46.496  1.00  0.00
ATOM     79 2HD2 ASN 1 114      19.079 -20.336  47.869  1.00  0.00
ATOM     80  N   ASP 1 116      16.009 -21.817  48.288  1.00  0.00
ATOM     81  CA  ASP 1 116      16.037 -21.119  49.574  1.00  0.00
ATOM     82  C   ASP 1 116      15.396 -19.793  49.630  1.00  0.00
ATOM     83  O   ASP 1 116      15.774 -18.837  50.337  1.00  0.00
ATOM     84  CB  ASP 1 116      17.464 -20.968  50.072  1.00  0.00
ATOM     85  CG  ASP 1 116      18.319 -22.224  49.976  1.00  0.00
ATOM     86  OD1 ASP 1 116      18.006 -23.130  50.730  1.00  0.00
ATOM     87  OD2 ASP 1 116      19.236 -22.263  49.180  1.00  0.00
ATOM     88  H   ASP 1 116      16.323 -21.489  47.396  1.00  0.00
ATOM     89  N   ASP 1 117      14.372 -19.664  48.769  1.00  0.00
ATOM     90  CA  ASP 1 117      13.409 -18.653  49.009  1.00  0.00
ATOM     91  C   ASP 1 117      12.024 -19.105  48.641  1.00  0.00
ATOM     92  O   ASP 1 117      11.645 -19.083  47.471  1.00  0.00
ATOM     93  CB  ASP 1 117      13.801 -17.459  48.181  1.00  0.00
ATOM     94  CG  ASP 1 117      13.342 -16.211  48.889  1.00  0.00
ATOM     95  OD1 ASP 1 117      13.889 -15.978  49.966  1.00  0.00
ATOM     96  OD2 ASP 1 117      12.577 -15.397  48.399  1.00  0.00
ATOM     97  H   ASP 1 117      14.092 -20.522  48.339  1.00  0.00
END
```

Figure 4

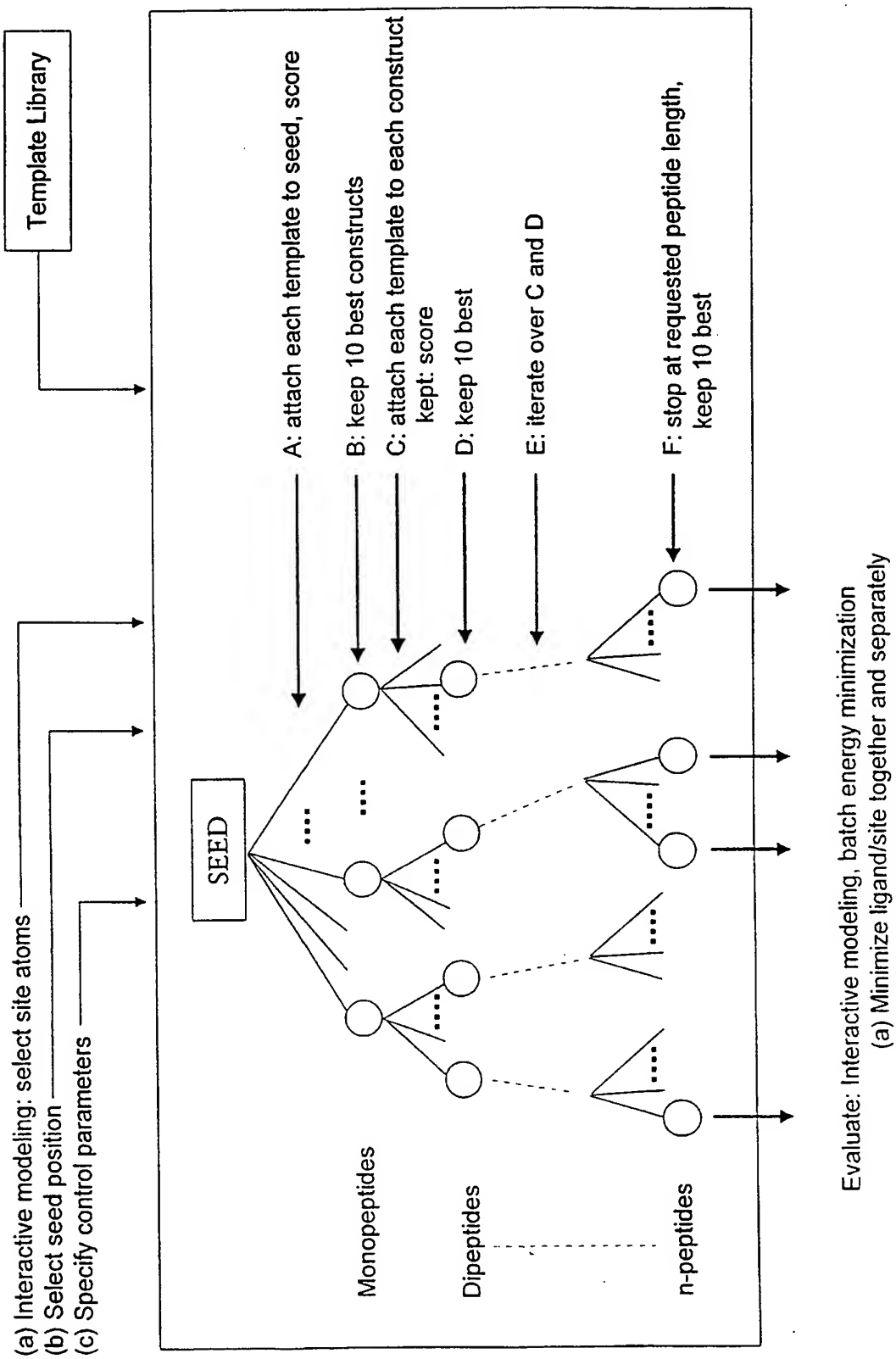

Template Library
(a) Interactive modeling: select site atoms
(b) Select seed position
(c) Specify control parameters
SEED
A: attach each template to seed, score
B: keep 10 best constructs
C: attach each template to each construct kept: score
D: keep 10 best
E: iterate over C and D
F: stop at requested peptide length, keep 10 best
Monopeptides
Dipeptides
n-peptides
Evaluate: Interactive modeling, batch energy minimization
(a) Minimize ligand/site together and separately
(b) Determine approximate binding energy

Figure 5

```
Human       Met Ala Leu Lys Arg Ile His Lys Glu Leu Asn Asp Leu Ala Arg Asp Pro Pro Ala Gln Cys Ser Ala Gly Pro Val Gly
S Pombe     Met Ala Leu Lys Arg Ile Asn Arg Glu Leu Ala Asp Leu Gly Lys Asp Pro Pro Ser Ser Cys Ser Ala Gly Pro Val Gly
C Albicans  Met Ser Leu Lys Arg Ile Asn Lys Glu Leu Ser Asp Leu Gly Arg Asp Pro Pro Ser Ser Cys Ser Ala Gly Pro Val Gly

            Asp Asp Met Phe His Trp Gln Ala Thr Ile Met Gly Pro Asn Asp Ser Pro Tyr Gln Gly Gly Val Phe Phe Leu Thr Ile
            Asp Asp Leu Phe His Trp Gln Ala Thr Ile Met Gly Pro Ala Asp Ser Pro Tyr Ala Gly Gly Val Phe Phe Leu Ser Ile
            Asp Asp Leu Tyr His Trp Gln Ala Ser Ile Met Gly Pro Pro Asp Ser Pro Tyr Ala Gly Gly Val Phe Phe Leu Ser Ile

            His Phe Pro Thr Asp Tyr Pro Phe Lys Pro Pro Lys Val Ala Phe Thr Thr Arg Ile Tyr His Pro Asn Ile Asn Ser Asn
            His Phe Pro Thr Asp Tyr Pro Phe Lys Pro Pro Lys Val Asn Phe Thr Thr Arg Ile Tyr His Pro Asn Ile Asn Ser Asn
            His Phe Pro Thr Asp Tyr Pro Leu Lys Pro Pro Lys Ile Ala Leu Thr Thr Lys Ile Tyr His Pro Asn Ile Asn Ser Asn


            Gly Ser Ile Cys Leu Asp Ile Leu Arg Ser Gln Trp Ser Pro Ala Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser
            Gly Ser Ile Cys Leu Asp Ile Leu Arg Asp Gln Trp Ser Pro Ala Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser
            Gly Asn Ile Cys Leu Asp Ile Leu Lys Asp Gln Trp Ser Pro Ala Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser


            Leu Leu Cys Asp Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala Arg Ile Tyr Gln Thr Asp Arg Glu Lys Tyr Asn
            Leu Leu Thr Asp Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His Val Tyr Lys Thr Asp Arg Ser Arg Tyr Glu
            Leu Leu Thr Asp Ala Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His Ile Tyr Lys Gln Asp Arg Lys Lys Tyr Glu


            Arg Ile Ala ArgGlu Trp Thr Gln Lys Tyr Ala Met
            Leu Ser Ala ArgGlu Trp Thr Arg Lys Tyr Ala Ile
            Ala Thr Ala LysGlu Trp Thr Lys Lys Tyr Ala Val
```

Figure 6

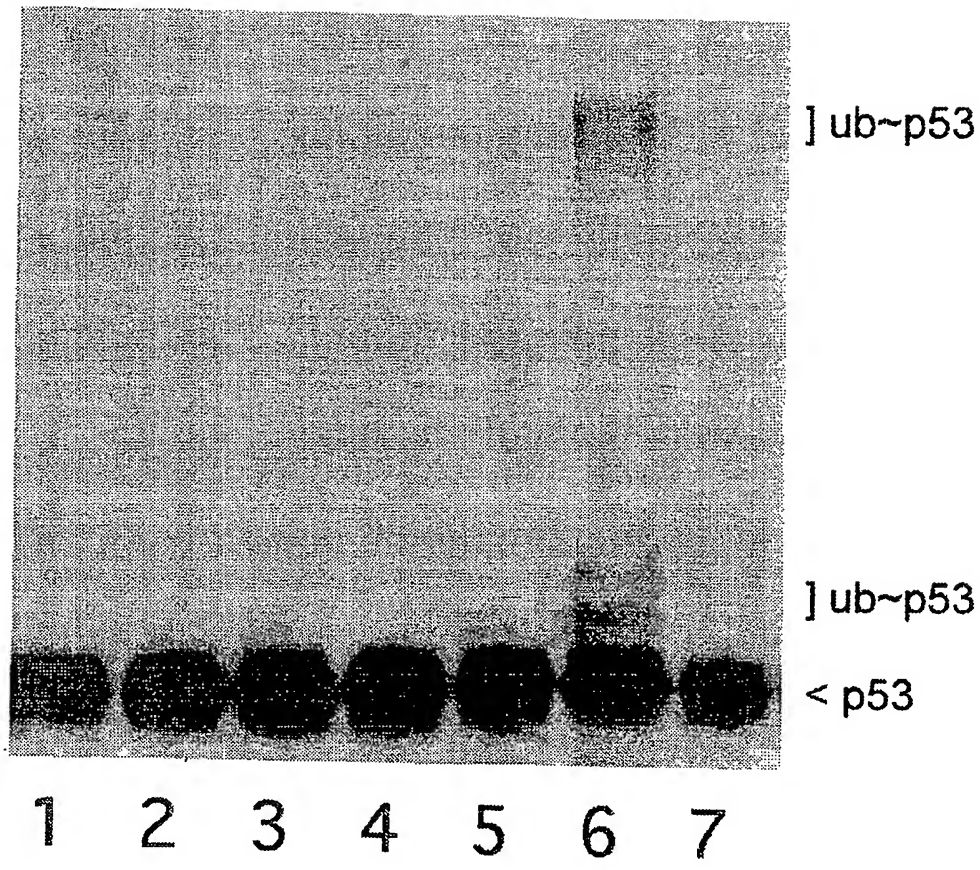
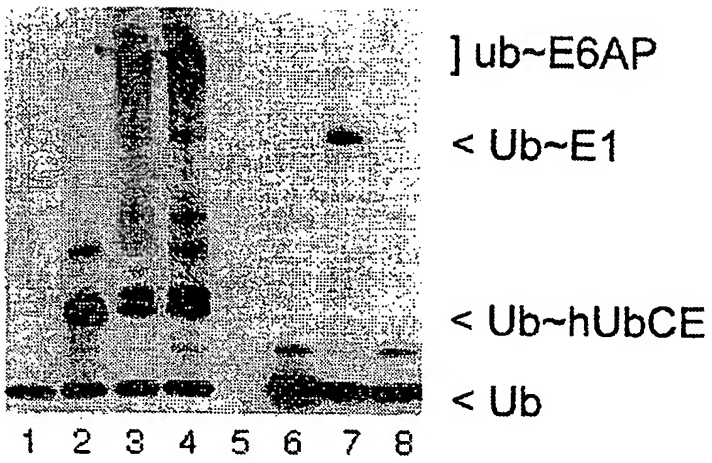


Figure 7A



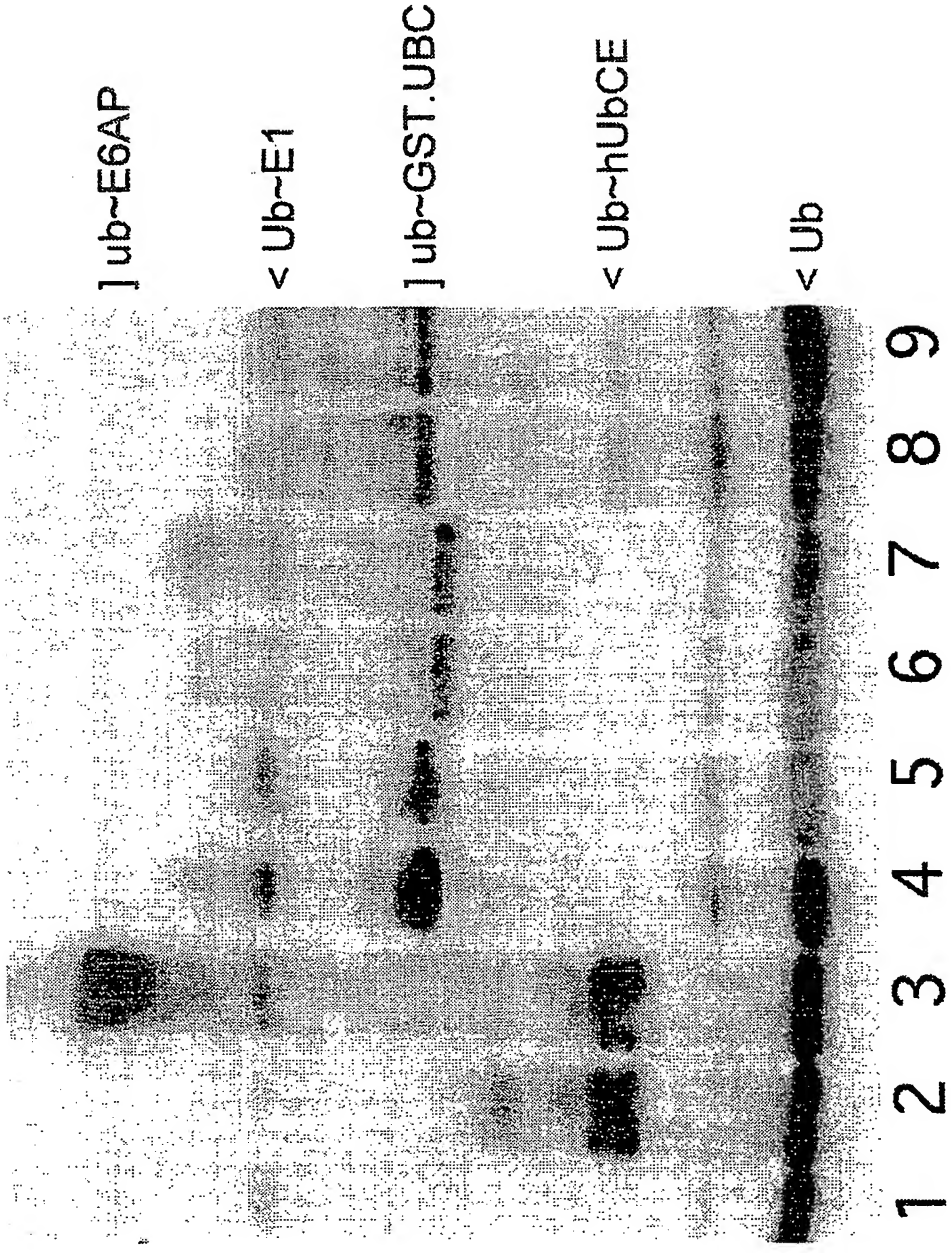


Figure 7B

Figure 8

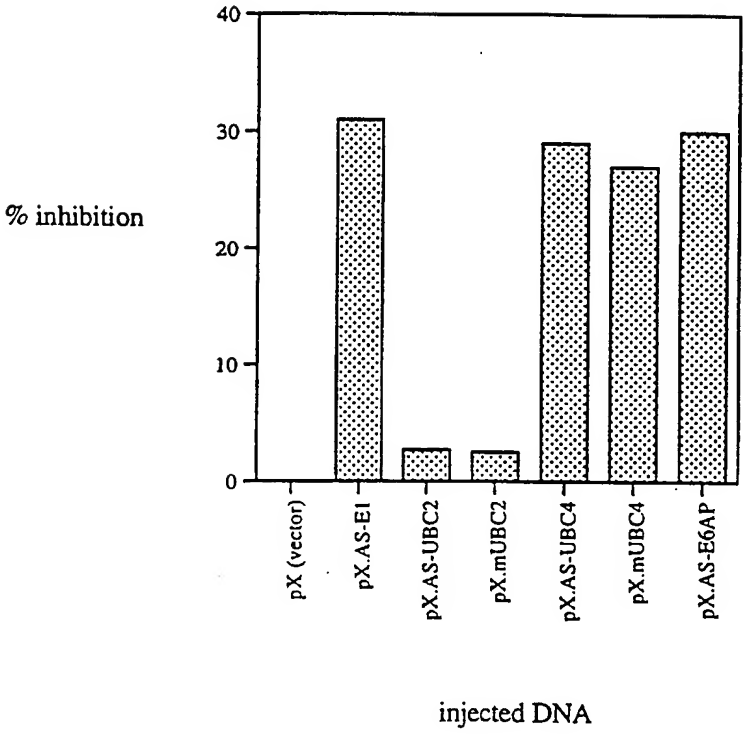
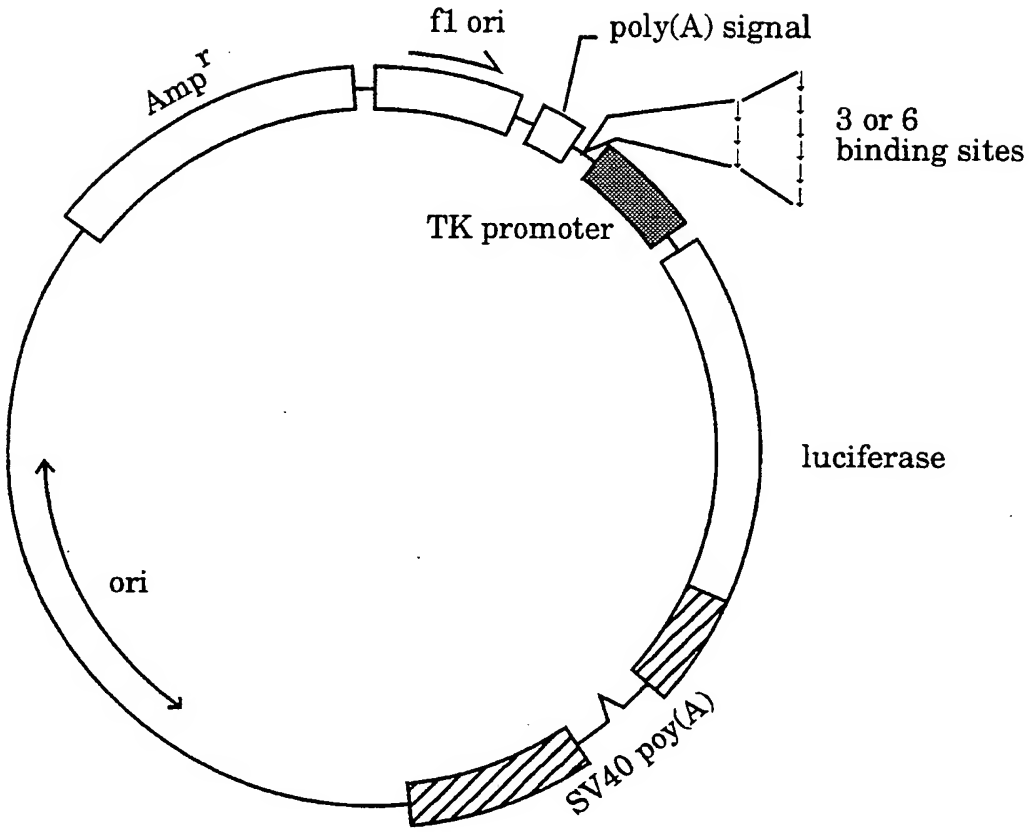

% inhibition
40
30
20
10
0
pX (vector)
pX.AS-E1
pX.AS-UBC2
pX.mUBC2
pX.AS-UBC4
pX.mUBC4
pX.AS-E6AP
injected DNA

Figure 9



p53 binding site: 5'-TCGACGGACATGCCCGGGCATGTCCC-3'
3'-GCCTGTACGGGCCCGTACAGGGACGCT-5'

myc binding site: 5'-TCGACCACGTGGC-3'
3'-GGTGCACCGAGCT-5'

Sp1 binding site: 5'-TCGACGGGGCGGGC-3'
3'-GCCCCGCCCGAGCT-5'